

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:15:18 ; Search time 58.56 seconds  
(without alignments)  
1126.671 Million cell updates/sec

Title: US-09-700-293-2

Perfect score: 3019

Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNRGRFGASVGYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3019	100.0	594	AAV23740	A surface protein
2	3019	100.0	594	AAV57044	BASB029 amino acid
3	3019	100.0	594	AAU06174	N. meningitidis EG
4	2874	95.2	594	AAU23739	A surface protein
5	2874	95.2	594	AAU06179	N. meningitidis B2
6	2855	94.6	598	AAU23742	A surface protein
7	2855	94.6	598	AAU06177	N. meningitidis H1
8	2852	94.5	598	AAU23738	A surface protein
9	2852	94.5	598	AAU06178	N. meningitidis B2
10	2783.5	92.2	591	AAV57045	BASB029 amino acid
11	2762.5	91.5	599	AAV23743	A surface protein

12	2762.5	91.5	599	22	AAU06176	N. meningitidis H3
13	2758.5	91.4	591	20	AAV27202	Amino acid sequenc
14	2758.5	91.4	591	20	AAV23746	A surface protein
15	2758.5	91.4	591	22	AAU06171	N. meningitidis PM
16	2751	91.1	592	20	AAV23737	A surface protein
17	2739.5	90.7	591	20	AAV23741	A surface protein
18	2739.5	90.7	591	22	AAU06175	N. meningitidis EG
19	2636	87.3	592	20	AAV23744	A surface protein
20	2636	87.3	592	22	AAU06172	N. meningitidis H4
21	2533	83.9	592	22	AAU06180	N. meningitidis H2
22	2516.5	83.4	589	20	AAV23745	A surface protein
23	2516.5	83.4	589	22	AAU06173	N. meningitidis P2
24	2504	82.9	592	20	AAU27203	Amino acid sequenc
25	2449	81.1	512	22	AAU06182	N. meningitidis PM
26	2409.5	79.8	513	22	AAU06183	N. meningitidis H4
27	2366	78.4	502	22	AAU06186	N. meningitidis PM
28	2230	73.9	604	22	AAU06181	N. meningitidis su
29	2032.5	67.3	433	22	AAU06185	N. meningitidis PM
30	1887.5	62.5	407	22	AAU06184	N. meningitidis PM
31	1328.5	44.0	2353	17	AAV99393	Haemophilus influe
32	1292.5	42.8	2411	21	AAV23860	Haemophilus influe
33	1055	34.9	1094	21	AAV23858	Haemophilus influe
34	1050	34.8	245	20	AAV27201	Amino acid sequenc
35	1030	34.1	1098	17	AAV99392	Haemophilus adhesi
36	978.5	32.4	679	17	AAV99394	Haemophilus influe
37	978.5	32.4	679	21	AAV23855	Haemophilus influe
38	741	24.5	1004	21	AAV23857	Haemophilus influe
39	727	24.1	1002	21	AAV23854	Haemophilus influe
40	689	22.8	1104	21	AAV23856	Haemophilus influe
41	689	22.8	1104	21	AAV23859	Haemophilus influe
42	595	19.7	116	21	AAV37832	Neisserial conserv
43	394.5	13.1	2314	22	AAV69136	M. catarrhalis les
44	393.5	13.0	1992	17	AAV04505	Moraxella 200 kDa
45	393.5	13.0	1992	22	AAV69133	M. catarrhalis str

#### ALIGNMENTS

RESULT 1  
AAV23740  
ID AAV23740 standard; Protein; 594 AA.  
XX AC AAV23740;  
XX DT 08-SEP-1999 (first entry)  
XX DE A surface protein of Neisseria meningitidis.  
XX KW Surface protein; surface glycoprotein; infection; vaccine;  
XX KW Immunoreactive peptide.  
XX OS Neisseria meningitidis.  
XX PN WO9931132-A1.  
XX PD 24-JUN-1999.  
XX PF 14-DEC-1998; 98WO-AU01031.  
XX PR 12-DEC-1997; 97GB-0026398.  
XX PA (ISIS-) ISIS INNOVATION LTD.  
XX PA (UYQU ) UNIV QUEENSLAND.  
XX PI Jennings MP, Moxon ER, Peak IRA;  
XX DR WPI; 1999-418754/35.  
XX DR N-PSDB; AAX85792.  
XX PT Neisseria meningitidis surface proteins useful for treating N.  
XX PT meningitidis infections

PS Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*

CC meningitidis which is approximately 62 kDa. The *N. meningitidis*

CC a thermostable polymers, nucleic acids, the primers and optionally

CC the detection of diagnosis of *N. meningitidis* infection in humans.

CC The *N. meningitidis* surface glycoproteins can also be used to

CC prevent or treat *N. meningitidis* infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;

XX Query Match 100.0%; Score 3019; DB 20; Length 594;

XX Best Local Similarity 100.0%; Pred. No. 5.1e-173;

XX Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKYRIIWSALNANWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60

DB 1 mnkyriiwsalnawavseltrnhtkrasatvavlatlilfatvqasttdddddyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTFAGTITLKAGDNLKIKQNTNE 120

DB 61 pvqrtavvlsfrsdkegtekevtesdnmgvyfdkkgvltagtitlkagdnlikqntne 120

QY 121 NTNASSFTYSLKKDLTDLTSVGTGKLSFNSANSKNVITSDTKGLNFAKKTAEETGDTTVH 180

DB 121 ntnassftyslkkdltdltsvgtgklsfnsansknvitsdtkglnfakktaeetgdttvh 180

QY 181 LNKGSTLTDLTLNAGTATVNDVNDDEKRAASVDVNLNAGNIGKVGPGTASDNV 240

DB 181 lnggstltdlntnagatvndvndvnddekkraasvdkvnlagnigkvgpgttasdnv 240

QY 241 DFVRYDYVEFISADTKTTNVESKONGKTEVTKIGAKTSVKEKDLVTKGDKGEND 300

DB 241 dfvrydyvefisadtkttnvveskngkrtvtekgaktsvikekdlvtkgdkgend 300

QY 301 SSTDKGGLYTAKEVIDAVNAGRWMTTANGQTGQADKFTVYSGNTVTFASGKTGA 360

DB 301 sstdkzgltyakevidavnnagrwmttlangqtgqadkfetvsgntvtfasgkgtta 360

QY 361 TVSKDDGNTVMYDVGNDALNVNQLONGWNLDSKAVAGSGKVGISGNVSPSKGRMDE 420

DB 361 tvskddgntvmvydvgndalnvnnqlongwnldskavagsgkvgisgnvpskgrmde 420

QY 421 TVNINAGNIEITRNGKNIDTATSMTPQFSVSLGAGADAPTLSDVEGALNVGSKDANK 480

DB 421 tvninagnieitrngknidiatstmpqfssvslgagadaptlsvddegalnvgskdank 480

QY 481 PVRITNAPGKEGDTNVAQLKGVAQNLNHNDVNDGNARAGIAQATATAGLVQAYLPG 540

DB 481 pvrtnvapgkegdtnvnaqlkgvaqnlndvndgnaragiatataglvqaylpg 540

QY 541 KSMMAIGGGTYRGEAGYATGYSSISDGGNIIKGTASGNSRHFASASVGYQW 594

DB 541 ksmmaigggtyrgeagyalgyssisdggnwlikgtasgnsrghfagasvgyqw 594

RESULT 2

AA57044

ID AA57044 standard; Protein; 594 AA.

XX AA57044;

XX 21-FEB-2000 (first entry)

XX BASB029 amino acid sequence from *N. meningitidis* strain ATCC13090.

XX BASB029; *Neisseria meningitidis*; surface fibril protein; HSP; diagnosis;

XX infection; treatment; prevent; antibacterial drug.

OS *Neisseria meningitidis*.

XX Key Location/Qualifiers

FT Misc-difference 104 /note= "Encoded by AATC"

XX WO9958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Ruelle J;

XX WPI: 2000-053103/04.

XX N-PSDB; AAZ39864.

PT New polypeptide from *neisseria meningitidis* useful for diagnosis,

XX treatment or prevention of bacterial infections in mammal

XX Claim 4; Fig 2; 74pp; English.

XX This is the *Neisseria meningitidis* BASB029 amino acid sequence from

CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the

CC *Haemophilus influenzae* surface fibrin (HSF) protein. The invention

CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and

CC polypeptide sequences (AAZ37044-Z37045) and their immunogenic fragments.

CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*

CC meningitidis infection in a mammal. Compositions containing an immune

CC polynucleotides and polypeptides are useful for generating an immune

CC response in an animal. A therapeutic composition comprising an antibody

CC directed against BASB029 is useful in treating humans with *Neisseria*

CC meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an

CC infection which results from increased or decreased expression of the

CC polynucleotide, and for therapeutic or prophylactic purposes.

CC particularly genetic immunisation. Antibodies against BASB029

CC polynucleotides and polypeptides are also useful for treating infections

CC particularly bacterial infections. The protein is useful in the

CC screening and development of antibacterial drugs. Fused recombinant

CC protein is useful for the stimulation of the immune system of an organism

CC receiving the protein.

XX Sequence 594 AA;

Query Match 100.0%; Score 3019; DB 21; Length 594;

Best Local Similarity 100.0%; Pred. No. 5.1e-173;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKYRIIWSALNANWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60

DB 1 mnkyriiwsalnawavseltrnhtkrasatvavlatlilfatvqasttdddddyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTFAGTITLKAGDNLKIKQNTNE 120

DB 61 pvqrtavvlsfrsdkegtekevtesdnmgvyfdkkgvltagtitlkagdnlikqntne 120

QY 121 NTNASSFTYSLKKDLTDLTSVGTGKLSFNSANSKNVITSDTKGLNFAKKTAEETGDTTVH 180

DB 121 ntnassftyslkkdltdltsvgtgklsfnsansknvitsdtkglnfakktaeetgdttvh 180

QY 181 LNKGSTLTDLTLNAGTATVNDVNDDEKRAASVDVNLNAGNIGKVGPGTASDNV 240

DB 181 lnggstltdlntnagatvndvndvnddekkraasvdkvnlagnigkvgpgttasdnv 240

QY 241 DFVRYDYVEFISADTKTTNVESKONGKTEVTKIGAKTSVKEKDLVTKGDKGEND 300

DB 241 dfvrydyvefisadtkttnvveskngkrtvtekgaktsvikekdlvtkgdkgend 300



QY 301 SSTDKGGLVTAKEVIDAVNKAGWRMKTITANGOTGQADKFETVTSCTNVTFSAGKGTGA 360  
 Db 301 sstkgeglvtakevidavnkagwrmtttangtqgqadkfetvtsntvtfasgkgtta 360  
 QY 361 TVSKDDGNTVMYDVNVGDALNVNQLONGWNLDKSAVAGSSGKVISGNVSPSKGKME 420  
 Db 361 tvskddgntvmymydvngdnlvnnqlngwnldskavagssgkvlsnvnspskgkme 420  
 QY 421 TVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480  
 Db 421 tvninagnnieitrngknidatsmtppqfssvslgagadaptlsvdddegalnvsgkdank 480  
 QY 481 PVRIITNAPGVKEGDTVNVNQAOLKGVNQLNHNHIDVNDGNARAGIAQAIATAGLVQAYLPG 540  
 Db 481 pvritnvpagvkegdvtnvaqlkgvaqnlhnhidvndgnaraglaiaataglvqaylpg 540  
 QY 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
 Db 541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 3  
 AAU06174  
 ID AAU06174 standard; Protein; 594 AA.  
 XX AC  
 XX AAU06174;  
 DT 24-OCT-2001 (first entry)  
 XX N. meningitidis EG327 surface antigen NhhA polypeptide sequence.  
 DE Surface antigen NhhA; meningococcal disease; meningitis vaccine.  
 KW Neisseria meningitidis strain EG327.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT Region 51..104  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT Region 105..116  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT Region 117..126  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT Region 127..190  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT Region 191..212  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT Region 213..231  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT Region 232..238  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT Region 239..594  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 XX WO200155182-A1.  
 PN  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-AU000069.  
 XX  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX

(UYQU ) UNIV QUEENSLAND.  
 PA  
 XX Peak IRA, Jennings MP;  
 PI  
 XX WPI; 2001-488774/53.  
 DR N-PSDB; AAS09164.  
 XX  
 XX New NhhA surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 preventing broad spectrum of Neisseria meningitidis -  
 XX Claim 9; Fig 1; 91pp; English.  
 PS  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen NhhA  
 CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen NhhA  
 CC from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX Sequence 594 AA;  
 SQ

Query Match 100.0%; Score 3019; DB 22; Length 594;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-173;  
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLFLPATVOASTDDDDLYLE 60  
 Db 1 mnkiyriiwsalnawavseltrnhtrkrasatvatvatlflfatvgastddddlyle 60  
 QY 61 PVQRTAVLSFRSDEKTEGKEVTEDSNWGVYFDKGLVGTAGTITLKAGDNLKIKQNTNE 120  
 Db 61 pvqrtavlsfrsdekgtgektevtedsnwgvfyfdkgkglvtagtittlkagdnllkikqntne 120  
 QY 121 NTNASFTYSLKDLTDLTSLVGTSEKLSFNSANSKNVNTSDTKFLNFAKKTAEETGDTTVH 180  
 Db 121 ntnasftyslkkdltdltsvgtseklfsfnsansknvntsdtkglnfakktaeetgdtvvh 180  
 QY 181 LINGIGSTLTDPLLTGATTVNTDNDVDEKKRAASVKDVLNAGWNKGVKPGGTASDNV 240  
 Db 181 lngigstltdtllntgattvntdndvdekkraasvkdvltnagwnlkgvpggtasdnv 240  
 QY 241 DFVRTYDVEFLSADTKTTTVNVESKONGKRTVEVKIGAKTSVIEKDKGLVTGDKGEND 300  
 Db 241 dfvrtydveflsadtktttvnnveskngkrtvevkigaktsviekdkglvtgdkgend 300  
 QY 301 SSTDKGGLVTAKEVIDAVNKAGWRMKTITANGOTGQADKFETVTSCTNVTFSAGKGTGA 360  
 Db 301 sstkgeglvtakevidavnkagwrmtttangtqgqadkfetvtsntvtfasgkgtta 360  
 QY 361 TVSKDDGNTVMYDVNVGDALNVNQLONGWNLDKSAVAGSSGKVISGNVSPSKGKME 420  
 Db 361 tvskddgntvmymydvngdnlvnnqlngwnldskavagssgkvlsnvnspskgkme 420  
 QY 421 TVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480  
 Db 421 tvninagnnieitrngknidatsmtppqfssvslgagadaptlsvdddegalnvsgkdank 480  
 QY 481 PVRIITNAPGVKEGDTVNVNQAOLKGVNQLNHNHIDVNDGNARAGIAQAIATAGLVQAYLPG 540  
 Db 481 pvritnvpagvkegdvtnvaqlkgvaqnlhnhidvndgnaraglaiaataglvqaylpg 540  
 QY 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
 Db 541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

Db 541 ksmmaigggtyrgeaygaigysldsgnwlktagnsrghfgasasvyyqw 594

RESULT 4  
 AAY23739  
 ID AAY23739 standard; Protein; 594 AA.  
 AC  
 AC AAY23739;  
 DT 08-SEP-1999 (first entry)  
 DE A surface protein of *Neisseria meningitidis*.  
 KW Surface protein; surface glycoprotein; infection; vaccine;  
 KW immunoreactive peptide.  
 OS *Neisseria meningitidis*.  
 FN WO9931132-A1.  
 PD 24-JUN-1999.  
 PF 14-DEC-1998; 98WO-AU01031.  
 PR 12-DEC-1997; 97GB-0026398.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UTQU) UNIV QUEENSLAND.  
 XI Jennings MP, Moxon ER, Peak IRA;  
 DR WPI: 1999-418754/35.  
 DR N-PSDB; AAX85791.  
 XX *Neisseria meningitidis* surface proteins useful for treating N.  
 PT meningitidis infections  
 PS Claim 1; Page 95-97; 132pp; English.  
 CC The present sequence represents a surface protein of *Neisseria*  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;  
 SQ

Query Match 95.2%; Score 2874; DB 20; Length 594;  
 Best Local Similarity 95.6%; Pred. No. 2.5e-164;  
 Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps

QY 1 MNKYYITWNSALNANVAVSELTRNHTKRASATVAVLATLILFATVQASTDDDDLYLE 60  
 Db 1 mnkyyitwnsalnnavvseltrnhtkrasatvavlatlilfatvqanatdddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTGKEVTEDSNNGVYFDKGVLTACTITLKAGONLIKONTNE 120  
 Db 61 pvqrtavvlsfrsdegtgekedtsnnavvyfdkrvfkagaitkagonlikontne 120

QY 121 NTWASFTYSLKDLTDLTISVGTKEKLSFSANSKNVNTSDTKGLNFAKTAETNGTGVH 180  
 Db 61 pvqrtavvlsfrsdegtgekedtsnnavvyfdkrvfkagaitkagonlikontne 180

QY 121 ntndsftyslkdltdltisvgtkeklslfsangknvntsdtkglnfaketaetngtpvh 180  
 Db 121 ntndsftyslkdltdltisvgtkeklslfsangknvntsdtkglnfaketaetngtpvh 180

QY 181 LNGIGSLTDLLNTGATVNTVNDNYTDDKKRAASVKQVLNAGNNIKGYPGTTASDNV 240  
 Db 181 lngigsltdllntgatvntvndnytddekkraasvkvdlngagwnlkgvkgpgttasdnv 240

Db 181 lngigsltdllntgatvntvndnytddekkraasvkvdlngagwnlkgvkgpgttasdnv 240

241	Db	dfrtydytveflsadtktttnvveskdngkktvfigaktsvikekdqglvrgkgkdeng	300
301	Qy	SSTDKCEGLVTAKEVIDAVANKAGWRMKTTTANGOTGQADKFETVTSGTNVTFASGKCTTA	360
360	Db	SSTDKEGLVTAKEVIDAVNKAGWRMKTTTANGTGTGQDKFETVSGCNVTFASGKCTTA	360
361	Qy	TVSKSDQGNITVMYDVNVGDALNVNOLNSGWNLDKSAVAGSSGKVGISGNVSPSGKMDK	420
420	Db	TVSKDQGNITVKYDNNVGDALNVGLNQSNGWNLDKSAVAGSSGKVGISGNVSPSGKMDK	420
480	Qy	TVNINAGNIEITRNGKNIDIAATSMTPQSSSVSLGAGADAPTLISVDDEGALNVGSKDANK	480
480	Db	TVNINAGNIEITRNGKNIDIAATSMTPQSSSVSLGAGADAPTLISVDDEGALNVGSKDANK	480
540	Qy	PVRITNVAPGKRGDVTNVAOLKGAONLNHNIDINVDGNARAGIAQATATAGLVQAVYLP	540
540	Db	PVRITNVAPGKRGDVTNVAOLKGAONLNHNIDINVDGNARAGIAQATATAGLVQAVYLP	540
594	Qy	KSMMAIGGNYRGEAGYAGYAGYSSIDGNNWIKGTASGNSRHRGASASVGVQW	594
594	Db	KSMMAIGGNYRGEAGYAGYAGYSSIDGNNWIKGTASGNSRHRGASASVGVQW	594
RESULT 5			
AAU061679 standard; Protein: 594 AA.			
ID	XX	AAU061679;	
AC	XX	AAU061679;	
DT	XX	24-OCT-2001 (first entry)	
DE	XX	N. meningitidis BZ198 surface antigen Nhma polypeptide sequence.	
DE	XX	Surface antigen Nhma; meningococcal disease; meningitis vaccine.	
KW	XX	Neisseria meningitidis strain BZ198.	
OS	XX	Location/Qualifiers	
Key	XX	1..50	
FH	XX	/label= C1	
FT	XX	/note= "Conserved region 1"	
FT	XX	51..104	
FT	XX	/label= V1	
FT	XX	/note= "Variable region 1"	
FT	XX	105..116	
FT	XX	/label= C2	
FT	XX	/note= "Conserved region 2"	
FT	XX	117..126	
FT	XX	/label= V2	
FT	XX	/note= "Variable region 2"	
FT	XX	127..190	
FT	XX	/label= C3	
FT	XX	/note= "Conserved region 3"	
FT	XX	191..212	
FT	XX	/label= V3	
FT	XX	/note= "Variable region 3"	
FT	XX	213..231	
FT	XX	/label= C4	
FT	XX	/note= "Conserved region 4"	
FT	XX	232..238	
FT	XX	/label= V4	
FT	XX	/note= "Variable region 4"	
FT	XX	239..594	
FT	XX	/label= C5	
FT	XX	/note= "Conserved region 5"	
XX	XX	WO200155182-A1.	
PN	XX	02-AUG-2001.	
PD	XX	25-JAN-2001; 2001WO-AU00069.	
PP	XX		

PR 25-JAN-2000; 2000US-0177917.  
PA (UYOU ) UNIV QUEENSLAND.  
PI Peak IRA, Jennings MP;  
XX WPI; 2001-488774/53.  
DR N-PSDB; AAS09169.  
XX New NhA surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX Claim 9; Fig 1; 91pp; English.  
PS The present invention relates to the isolation of novel Neisseria  
XX meningitidis mutant polypeptides of the surface antigen NhA  
CC (AAU06182-AAU06186). The modified or mutant NhA polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen NhA  
CC from N. meningitidis strain B2198 is 1 of 10 NhA polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
XX the present invention.  
XX Sequence 594 AA;  
SQ

Query Match 95.2%; Score 2874; DB 22; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.5e-164;  
Matches 566; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWVAVSELNRHTRKASATVATVATLTLFATVQASTTDDDDLYLE 60  
Db 1 mnkiyriiwsalnawvavselnrhtrkrasatvatavlatllfatvqanatdddlyle 60

QY 61 PVQRTAVVLSFRSDEKTEGKEVTEDSNMGVYFDKGVLTAGTITLTKAGNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdektegkedgednawwyfdekrvklagaitlkgadnlkikqntne 120

QY 121 NTNASSFTYSLLKDLTDLTSVGTSEKLSFNSANSKNVITSDTKGLNFAKKTAEITNGDTTVH 180  
Db 121 ntndssftysllkdltltsveteklsfgangknvitsdtkglnfakctagntngdptvh 180

QY 181 LINGIGSLTDTLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNKGVKPGTASDNV 240  
Db 181 lngigsltdtllntgattntvndvndtdekkraasvkdvlngagwnkvgkpgttdsnv 240

QY 241 DFVITYDTVFLSADTTTNNVESKONGKRTVEKIGAKTSVTEKDGKLVTKGKXGEND 300  
Db 241 dfvitydtvflsadttnnnveskdngkrtvekvigaktsvtekdqkivtgkgkdng 300

QY 301 SSTDKGELVTAKEVIDAVNKAQWRMTTANGOTGOADKEFTVTSCTNVTFRASGKGTTA 360  
Db 301 sstdkgelvtakevidavnkagwrmtttangotgoadkfevtvtsqntvtfasgkgtta 360

QY 361 TVSKDDGNTITVMYDVNNGDALNVLQNSGNLDSKAVAGSSGKVSIGNVSPSKGKMD 420  
Db 361 tvskddgntitvmydvnnvgdalnvnqlqnsqgnldskavagsgkvisgnvpskqkmd 420

QY 421 TVNINAGNIEITRNKNIDIAATSMTPQFSVSLGAGADAPTILSVDDGALNVGSKDANK 480  
Db 421 tvninagnieitrngnkniatsmapqfssvslgagadaptilsvddgalnvgskdtnk 480

QY 481 PVRITNVPAGVKEGDVTNVAQLKVAQNLNHIDNVGNRAGIAQAIATAGLVQAYLPG 540  
Db 481 pvrtnvpagvkegdvtnvaqlkgvaqnlndvndvgnragiaqaiataglvqaylpg 540

QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594  
Db 541 ksmmaiggyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw 594

RESULT 6  
AAY23742  
ID AAY23742 standard; Protein; 598 AA.  
XX AC AAY23742;  
XX DT 08-SEP-1999 (first entry)  
XX DE A surface protein of Neisseria meningitidis.  
XX KW Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX OS Neisseria meningitidis.  
XX PN WO9931132-A1.  
XX PD 24-JUN-1999.  
XX PF 14-DEC-1998; 98WO-AU01031.  
XX PR 12-DEC-1997; 97GB-0026398.  
XX PA (ISIS-) ISIS INNOVATION LTD.  
XX PA (UYOU ) UNIV QUEENSLAND.  
XX PI Jennings MP, Moxon ER, Peak IRA;  
XX WPI; 1999-418754/35.  
XX DR N-PSDB; AAX85794.  
XX PT Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX Claim 1; Page 108-110; 132pp; English.  
XX CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX Sequence 598 AA;  
SQ

Query Match 94.6%; Score 2855; DB 20; Length 598;  
Best Local Similarity 94.6%; Pred. No. 3.4e-163;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVAVSELNRHTRKASATVATVATLTLFATVQASTTDDDDLYLE 60  
Db 1 mnkiyriiwsalnawvavselnrhtrkrasatvatavlatllfatvqanatdddlyle 60

QY 61 PVQRTAVVLSFRSDEKTEGKEVTEDSNMGVYFDKGVLTAGTITLTKAGNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdektegkedgednawwyfdekrvklagaitlkgadnlkikqntne 120

QY 121 NTNASSFTYSLLKDLTDLTSVGTSEKLSFNSANSKNVITSDTKGLNFAKKTAEITNGD 176  
Db 121 ntntndssftysllkdltltsveteklsfgangknvitsdtkglnfakctagntngd 180

QY 177 TTVHLNGIGSLTDTLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 181 ptvhlngigsltdtllntgattntvndvndtdekkraasvkdvlngagwnkvgkpgtta 240

Qy 237 SDNVDFVRYDTVEFLSADTKTTTNNVESKDNKRTVEVIGAKTSVIREKDKLVTGDK 296  
Db 241 sdndvfvrydtveflsadtktttvnnveskdngkktvevkgaktsvirekdklvtgkgk 300  
Qy 297 GENDSSTDKGEGLVTAKEVIDAVNKAQWRMKTATTANGQTGOADKFTETVTSCTNTVTFASGK 356  
Db 301 dengsstdegeglvtakevidavnkagwrmtttangqtgqadkfetvtsktvtfasgn 360  
Qy 357 GTTATVSKDDQGNITVMYDVMVGNLQNSGNWLDKAVAGSSGKVLISGNVSPSKG 416  
Db 361 gttatvskddqgnitvmydvmvgnlqnsqwnldskavagssgkvlisgnvpskg 420  
Qy 417 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 421 kmdetvniagnnieitrngknidiatmtpfssvslgagadaptlsvddegalnvgsk 480  
Qy 477 DANKPVRTITNAPGVKEDVTNVAQLKGVQNLNNHIDVGNRAGTAQAIATAGLVQA 536  
Db 481 dankpvrtnapgvkedvtvnvaqlkgvqnlnnhridvgnrnagtaqaiataglaqa 540  
Qy 537 YLPKGSMAIGGTVRGAGYAIGYSSISDGGNWIIGTPASNSRGHFGASASVGYQW 594  
Db 541 ylpkgsmaiggtvrgagyaigyssisdggnwiigtptasnsrghfgasasvgyqw 598

RESULT 7  
AAU06177  
ID AAU06177 standard; Protein; 598 AA.  
XX AC AAU06177;  
XX DT 24-OCT-2001 (first entry)  
XX DE N. meningitidis H15 surface antigen Nhma polypeptide sequence.  
XX KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
XX OS Neisseria meningitidis strain H15.  
XX FH Key  
FT Region 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..104  
FT /label= V1  
FT /note= "Variable region 1"  
FT 105..116  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 117..130  
FT /label= V2  
FT /note= "Variable region 2"  
FT 131..194  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 195..216  
FT /label= V3  
FT /note= "Variable region 3"  
FT 217..235  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 236..242  
FT /label= V4  
FT /note= "Variable region 4"  
FT 243..598  
FT /label= C5  
FT /note= "Conserved region 5"  
XX WO200155182-A1.  
XX PD 02-AUG-2001.  
XX

PF 25-JAN-2001; 2001WO-AU00069.  
XX 25-JAN-2000; 2000US-0177917.  
PR (UYQU ) UNIV QUEENSLAND.  
XX Peak IRA, Jennings MP;  
XX WPI: 2001-488774/53.  
XX N-PSDB; AAS09167.  
XX New Nhma surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX Claim 9; Fig 1; 9lpp; English.  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhma  
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC immunisants. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhma  
CC from N. meningitidis strain H15 is 1 of 10 Nhma polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
XX the present invention.  
SQ Sequence 598 AA;  
Query Match 94.6%; Score 2855; DB 22; Length 598;  
Best Local Similarity 94.6%; Pred. No. 3 4e-163;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
Qy 1 MNKIYIITWNSALNANVAVSELFRNHTKKRASATVATVATLFLFATVQASTDDDDLYLE 60  
Db 1 mnkiyilwnsalnawvsvseltrnhtkrasatvavtavlflfatvqastdddddlyle 60  
Qy 61 PVQRTAVVLSFRSKEGTEGKEVTEDSNMGVDFKGVLTAGTITLKAGDNLIKQWNE 120  
Db 61 pvqrtavvlsfrskegtegkegtevtedsnmgvdfkgrvltagtitlkagdnlikqgnne 120  
Qy 121 NTNA----SSFTYSLKKDLTDLTSVGTPEKLSFSANSKNVNTSDTKGLNFAKTAETNGD 176  
Db 121 ntntndssftyslkkdldtldtsveteklsfsgangknvntsdtkglnfaketaetngd 180  
Qy 177 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGNNIKGVKPGTTA 236  
Db 181 ptvhlngigstltdtllntgattntvndnvtddkkraasvkdvlnagwnikgvkpgtta 240  
Qy 237 SDNVDFVRYDTVEFLSADTKTTTNNVESKDNKRTVEVIGAKTSVIREKDKLVTGDK 296  
Db 241 sdndvfvrydtveflsadtktttvnnveskdngkktvevkgaktsvirekdklvtgkgk 300  
Qy 297 GENDSSTDKGEGLVTAKEVIDAVNKAQWRMKTATTANGQTGOADKFTETVTSCTNTVTFASGK 356  
Db 301 dengsstdegeglvtakevidavnkagwrmtttangqtgqadkfetvtsktvtfasgn 360  
Qy 357 GTTATVSKDDQGNITVMYDVMVGNLQNSGNWLDKAVAGSSGKVLISGNVSPSKG 416  
Db 361 gttatvskddqgnitvmydvmvgnlqnsqwnldskavagssgkvlisgnvpskg 420  
Qy 417 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 421 kmdetvniagnnieitrngknidiatmtpfssvslgagadaptlsvddegalnvgsk 480  
Qy 477 DANKPVRTITNAPGVKEDVTNVAQLKGVQNLNNHIDVGNRAGTAQAIATAGLVQA 536  
Db 481 dankpvrtnapgvkedvtvnvaqlkgvqnlnnhridvgnrnagtaqaiataglaqa 540

Db 481 dankpvrtnvapgvkegdvtnvaqlkgvaqnlmnrldnvdgnaraglaiaataglaqa 540  
Qy 537 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGTAGSGNRGHFGASASVGYQW 594  
Db 541 ylpkssmmaiggtyrgeagyaigysissdgtgnwviktagsgnrgfhfgasasvgyqw 598

RESULT 8  
AAU06178 standard; Protein; 598 AA.  
XX AC AAU06178;  
XX DT 24-OCT-2001 (first entry)  
XX DE N. meningitidis B210 surface antigen NhhA polypeptide sequence.  
XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.  
XX OS Neisseria meningitidis strain B210.  
XX PS Claim 1; Page 91-93; 132pp; English.  
XX CC The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

XX SQ Sequence 598 AA;  
Query Match 94.5%; Score 2852; DB 20; Length 598;  
Best Local Similarity 94.6%; Pred. No. 5.2e-163;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
Qy 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLFLFATVQASTDDDDLYLE 60  
Db 1 mnkisirwiwnsalnawvsvseltrnhtkrasatvatvatlflfatqanadddlyle 60  
Qy 61 PVQRTAVVLSRFSRKEGTEVEVDSNWGYFDKGVLTAGTITLRAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsrfsrkegtevedsnwgyfdkgrvltagtitlragnlklkqntne 120  
Qy 121 NTNA----SFTYSLKKDLTDLTSGTEKLSFNSANKVNITSDTKGLNFAKTAETNGD 176  
Db 121 ntntndtsrfsylskldltsgteklslfngankvnitstdtkglnfaktaetngd 180  
Qy 177 TTVHLNGIGSTLDTLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNKGVKPGTTA 236

Db 181 ptvhlnglsgltldtllntgattntndnvtddkkrasvkdvlmagwnlkgvkgpgtta 240  
Qy 237 SDNYDFVRYTDTVFELSDATKTTTNNVESKDNKRTEVKIGAKTSVKEKDKGLVTGDK 296  
Db 241 sdnydfvrytdtveflsadtktttnvveskdngkrtevkigaktsvikekdglvtgk 300  
Qy 297 GENDSSTDKGELVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFETVTSCTNTVTFASGK 356  
Db 301 gengsstdegeglvtakevidavnkagwrmttttangotgqadkfetvtsctktvfasgn 360  
Qy 357 GTTATVSKDDQGNITVMYDVMVGDALNVNQLNSGNWINDSKAVAGSSKVTISGNVSPSKG 416  
Db 361 gttatvskddqgnitvmydvmvvgdalnvnqlnsgwnlndskavagssgkvtsnvnspsgk 420  
Qy 417 KMDETVMINAGNNEITRNGKNIDIASTMTPOFSSVSLGACADAPTLSVDDDEGALNVGSK 476  
Db 421 kmdevtminagnnleitrngknidiatmtpqfssvslgagadaptsvdddegalnvgsk 480  
Qy 477 DANKPVRITNVAPGVKEGDVTVNAQLKGVAQNLNHHDNDVGNARAGIAQAIAATAGLVQA 536  
Db 481 dankpvrtnvapgvkegdvtnvaqlkgvaqnlmnrldnvdgnaraglaiaataglaqa 540  
Qy 537 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGTAGSGNRGHFGASASVGYQW 594  
Db 541 ylpkssmmaiggtyrgeagyaigysissdgtgnwviktagsgnrgfhfgasasvgyqw 598

RESULT 9  
AAU06178  
ID AAU06178 standard; Protein; 598 AA.  
XX AC AAU06178;  
XX DT 24-OCT-2001 (first entry)  
XX DE N. meningitidis B210 surface antigen NhhA polypeptide sequence.  
XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.  
XX OS Neisseria meningitidis strain B210.  
XX PS Key Location/Qualifiers  
XX FH 1..50  
XX FT /label= C1  
XX FT /note= "Conserved region 1"  
XX FT 51..104  
XX FT /label= V1  
XX FT /note= "Variable region 1"  
XX FT 105..116  
XX FT /label= C2  
XX FT /note= "Conserved region 2"  
XX FT 117..130  
XX FT /label= V2  
XX FT /note= "Variable region 2"  
XX FT 131..194  
XX FT /label= C3  
XX FT /note= "Conserved region 3"  
XX FT 195..216  
XX FT /label= V3  
XX FT /note= "Variable region 3"  
XX FT 217..235  
XX FT /label= C4  
XX FT /note= "Conserved region 4"  
XX FT 236..242  
XX FT /label= V4  
XX FT /note= "Variable region 4"  
XX FT 243..298  
XX FT /label= C5  
XX FT /note= "Conserved region 5"  
XX PN WO200155182-A1.  
XX



CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 92.2%; Score 2783.5; DB 21; Length 591;  
Best Local Similarity 93.3%; Pred. No. 6.5e-159;  
Matches 558; Conservative 9; Mismatches 20; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD--DDDL 57  
DB 1 mnklyriiwsalnawavseltrnhtrkrasatvktavlatcllfatvgasanegeedl 60  
QY 58 YLEPQRTAVVLSRDKGEGTGEKE-VTEPSNMGVYFDKKGVLTAGTITLKAGDNLIKQ 116  
DB 61 yldpqrvtavlivnsdkegkgevedsnwavydekglvtareitlkagdnlikq 120  
QY 117 NTNENTWASFTYSLKKDLTDLTSVGTSEKLSFNSANKVNITSDTKGLNFAKKTAEINGD 176  
DB 121 -----ngsnftyslkkdltdltsvgtekisfsangknvitsdtkglnfaketagngd 174  
QY 177 TTVHLNGIGSTLTDLTLTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 236  
DB 175 ttvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnlkvgkpgtta 234  
QY 237 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEDKGLVTGDK 296  
DB 235 sdnvdfvrytdtveflsadtktttvnnveskdngkrtevkigaktsvikekgklvtgdk 294  
QY 297 GENDSSDTKGEGVLTAKEVIDAVNKAQWRMKTNTTANGOTGQADKFEVTSCTNVTFAAGK 356  
DB 295 gendssdtkgeglvtakevidavnakagwrmttttangotgqadkfetvsgtnvtfasgk 354  
QY 357 GTTATVSKDDOQNTVMYDVNVGDALNVNQLQNSGWNLDKAVAGSGKVTSGNVSPSKG 416  
DB 355 gttatvskddqgnltvmymvngdnlvngvgnlqnsqwnldskavagsgkvtsngnvspkg 414  
QY 417 KMDETVMINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476  
DB 415 kmdevminagnnieitrngknidiatmtptqfssvslgagadaptilsvdgd-alnvgsk 473  
QY 477 DANKPVRITNVAPGVKEGDTVNAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQA 536  
DB 474 dnpkpvritnvapgvkegdvtnvaqlkgvaqnlhndvndgnaragiagaiaataglvqa 533  
QY 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNNI IKGTASGNSRGRHFGASASVGYQW 594  
DB 534 ylpcksmmaigggtyrgeagyaigyssisdggnwlikgtasgnsrgrhfgasasvgyqw 591

RESULT 11  
AAV23743  
ID AAV23743 standard; Protein; 599 AA.  
XX  
AC AAV23743;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX

PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI; 1999-418754/35.  
DR N-PSDB; AAX85795.  
XX  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PT  
XX Claim 1; Page 114-115; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 599 AA;  
Query Match 91.5%; Score 2762.5; DB 20; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.2e-157;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD-DDDL 59  
DB 1 mnklyriiwsalnawavseltrnhtrkrasatvktavlatcllfatvganadede 60  
QY 60 EPVQRTAVVLSRDKGEGTGEKEVTEPSNMGVYFDKKGVLTAGTITLKAGDNLIKQ--- 116  
DB 61 epvrsalvlqfmdlkegnesestgnlgwalyndhnlhgatvltkagdnlikqntn 120  
QY 117 -NTNENTWASFTYSLKKDLTDLTSVGTSEKLSFNSANKVNITSDTKGLNFAKKTAEING 175  
DB 121 kntentndssftyslkkdltdltsvetekisfsangknvitsdtkglnfaketagng 180  
QY 176 DTTVHLNGIGSTLTDLTLTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 235  
DB 181 dttvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnlkvgkpgtt 240  
QY 236 ASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEDKGLVTGKD 295  
DB 241 asdnvdfvrytdtveflsadtktttvnnveskdngkrtevkigaktsvikekgklvtgk 300  
QY 296 KGENDSSDTKGEGVLTAKEVIDAVNKAQWRMKTNTTANGOTGQADKFEVTSCTNVTFAAG 355  
DB 301 kgendssdtkgeglvtakevidavnakagwrmttttangotgqadkfetvsgtnvtfasg 360  
QY 356 KGTATVSKDDOQNTVMYDVNVGDALNVNQLQNSGWNLDKAVAGSGKVTSGNVSPSK 415  
DB 361 kgtatvskddqgnltvmymvngdnlvngvgnlqnsqwnldskavagsgkvtsngnvspsk 420  
QY 416 GKMDETVMINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGS 475  
DB 421 gkmdetvminagnnieitrngknidiatmtptqfssvslgagadaptilsvdkgalnvg 480  
QY 476 KDANKPVRITNVAPGVKEGDTVNAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQ 535  
DB 481 kdnpkpvritnvapgvkegdvtnvaqlkgvaqnlhndvndgnaragiagaiaataglvq 540  
QY 536 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNNI IKGTASGNSRGRHFGASASVGYQW 594

```

Db 541 aylpgksmmaiggytygeagyaigyssisdggnwikgtasgnrghfgasasvgyqw 599
|||||
RESULT 12
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX
AC AAU06176;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H38 surface antigen Nhha polypeptide sequence.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H38.
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..105
FT /label= V1
FT /note= "Variable region 1"
FT Region 106..117
FT /label= C2
FT /note= "Conserved region 2"
FT Region 118..131
FT /label= V2
FT /note= "Variable region 2"
FT Region 132..195
FT /label= C3
FT /note= "Conserved region 3"
FT Region 196..217
FT /label= V3
FT /note= "Variable region 3"
FT Region 218..236
FT /label= C4
FT /note= "Conserved region 4"
FT Region 237..243
FT /label= V4
FT /note= "Variable region 4"
FT Region 244..599
FT /label= C5
FT /note= "Conserved region 5"
XX
WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
WP1: 2001-488774/53.
DR N-PSDB; AAS09166.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in

```

```

CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 599 AA;

```

```

Query Match 91.5%; Score 2762.5; DB 22; Length 599;
Best Local Similarity 91.7%; Pred. No. 1.2e-157;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATATLTLFATVQASTTD-DDDLYL 59
Db 1 mnkiyriiwsalnawvavseltrnhtkrasatvktavlatllfatvqanattede 60
QY 60 EPVORTAVLWLSFRSDKEGTGEKVEDSDNWGVYDFDKKGLTAGTITLTKAGDNLKIQ--- 116
Db 61 epvrsalvlqfmdkeggenesnigwsiyydnhtlhgatvtlkgdnlkikqtn 120
QY 117 -NTNENTNASSFTYSLKDLTDLTSVGTKEKLSFSAANSKNYNTSDTKGLNFAKKTAE 175
Db 121 kntentndsftyslkkdldttsveteklsfgangknitsdtkglnfaketagtn 180
QY 176 DTTVHLNGICSTLTDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 235
Db 181 dtvhlngistltdtllntgattnvndvtdkkrasvkdvnagwnlkgvpgtt 240
QY 236 ASDNWDFVRYDYVFLSADTFTTVNVESKDNKRETVKIGAKTSVIEKDGKLVTKD 295
Db 241 asdnvdfvchtydceflvsadtkttnvveskdngkrkevkgaksviekdgkltv 300
QY 296 KGENSDSTDKGELVTAKEVIDAVNKGWRMKTMTTANGQTQADKPFETVTSNVTFFAG 355
Db 301 kgensstdegeglvtakevidavnkagwrnktttangqtgqadkfetvtsnvtf 360
QY 356 KGTATVSKDDQGNITMYDVMVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSK 415
Db 361 kgtatvskddqgnitvdydvmvgdalnvqlnsgwnldskavagssgkvisgnv 420
QY 416 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDKGA 475
Db 421 gkmdetvniagnnieitrngknidiatsmtppqfssvslgagadapltlsvdk 480
QY 476 KDANKPVRIITNAPGVKEGDTNVAOLKGVAQNLNNHIDNVGNRAGIAQAIATAG 535
Db 481 kdnkpvritnvapgvkegdtnvaolkgvaqnlndvgnrnridnvdgnaragiag 540
QY 536 AYLPGKSMMAIGGTYRGEAGYAIGYSSTSDGGNWIILKGTASNGRHFCASASVGY 594
Db 541 aylpgksmmaiggytyrgeagyaigyssisdggnwikgtasgnrghfgasasv 599

```

```

RESULT 13
AAU27202
ID AAU27202 standard; Protein; 591 AA.
XX
AC AAU27202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX bacterial infection; treatment.
XX
OS Neisseria meningitidis.
XX

```



PN W09936544-A2.  
XX 22-JUL-1999.  
XX 14-JAN-1999; 99WO-IB00103.  
XX 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX (CHIR-) CHIRON SPA.  
XX Grandi G, Masiagnani V, Pizza M, Rappuoli R, Scarlato V;  
PI WPI; 1999-444400/37.  
XX N-PSDB; AAX99124.  
DR New protein and its nucleotide sequence, useful in vaccines or  
XX diagnostic compositions for treating and/or preventing *Neisseria*  
PT meningitidis infections  
XX Claim 1; Page 62; 123pp; English.  
XX  
XX The invention provides proteins (AAY27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
XX  
XX Sequence 591 AA;  
SQ  
  
Query Match 91.4%; Score 2758.5; DB 20; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2e-157;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
  
Qy 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLTLFATVOASTD---DDL 57  
Db 1 mnkiyriiwnsalnawvvselttrnhtkrasatvktavlatllfatvqasannee 60  
  
Qy 58 YLEPVQRTAVVLSFRSKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLIKQ 116  
Db 61 yldpvqrtavvllvnsdskgektekveensdwavfnekvltareitlkagdnlikq 120  
  
Qy 117 NTNENTWASSFTYSILKDLTDLTSVGTKEKLSFSANSKNVITSDTKGLNFAKKTAE 176  
Db 121 -----ngtnftyslkkdltltsvgteklfsfsgangknvitsdtkglnfaketa 174  
  
Qy 177 TTVHLNGIGSLTDLTLNTGATTNVDNDVDEKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 ttvhlngigsltdlntgattnvdndvlddekkraasvkvlnagwnikgvpkgtta 234  
  
Qy 237 SDNVDFVRYTYDFELSDATTTTVNVESKNGRRTVEKIGAKTSVKEKDGKLVGTGDK 296  
Db 235 sdnvdfvrytydfeladtktttvnvskngdkkvekvigaktsvikekgdgvltgdk 294  
  
Qy 297 GENDSSDTDKGSLTAKEVIDAVNKAGRMKTTTANGOTGOADKFEETVSGTNVTFASG 356  
Db 295 gendssdegeglvtakevidavnkagwmktttangotgqadkfetvsgtnvtfasg 354  
  
Qy 357 GTTATVSKDDOGNTVMYDVNVGDALNVQLNSGNWLDLSKAVAGSSGKVTSGNVSPSKG 416  
Db 355 gttatvskddognltvmvdyvngdnlvnlqnsqwnldskavagssgkvlsngvpskg 414  
  
Qy 417 KMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSVSLGAGADAPTLSVDDDEAGNVSGK 476  
Db 415 kmdetvniagnnieitrngknidiatmtppqfssvslgagadapltsvddg-alnvsgk 473  
  
Qy 477 DANKPVRTITNVPAGVKEGDVTNVAQLKCAVQNLNHNIDVNGNARAGIAQAIAAGLVQA 536  
Db 474 kankpvrtnvpagvkegdvtnvaqlkgvaqnlhndvngnarnagiagaiaaglvqa 533

Qy 537 YLPKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFCASASVQYQW 594  
Db 534 ylpksmmaiggtgtyrgeagyaigyssisdgnwliiktasgnsrghfgasasvqyqw 591  
  
RESULT 14  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
XX AAY23746;  
AC  
XX 08-SEP-1999 (first entry)  
XX A surface protein of *Neisseria meningitidis*.  
DE Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
KW  
XX *Neisseria meningitidis*.  
OS  
XX W09931132-A1.  
PN  
XX 24-JUN-1999.  
PD  
XX 14-DEC-1998; 98WO-AU01031.  
XX  
XX 12-DEC-1997; 97GB-0026398.  
PR  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
XX *Neisseria meningitidis* surface proteins useful for treating *N.*  
PT meningitidis infections  
XX  
XX Claim 1; Page 127-128; 132pp; English.  
XX  
XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX Sequence 591 AA;  
SQ

Query Match 91.4%; Score 2758.5; DB 20; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2e-157;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
  
Qy 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLTLFATVOASTD---DDL 57  
Db 1 mnkiyriiwnsalnawvvselttrnhtkrasatvktavlatllfatvqasannee 60  
  
Qy 58 YLEPVQRTAVVLSFRSKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLIKQ 116  
Db 61 yldpvqrtavvllvnsdskgektekveensdwavfnekvltareitlkagdnlikq 120  
  
Qy 117 NTNENTWASSFTYSILKDLTDLTSVGTKEKLSFSANSKNVITSDTKGLNFAKKTAE 176  
Db 121 -----ngtnftyslkkdltltsvgteklfsfsgangknvitsdtkglnfaketa 174  
  
Qy 177 TTVHLNGIGSLTDLTLNTGATTNVDNDVDEKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 ttvhlngigsltdlntgattnvdndvlddekkraasvkvlnagwnikgvpkgtta 234



QY 417 KMDETVNIAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 476  
 Db 415 kmdetvniagnnieitrngknidiatsmtpqfssvslgagadaptlsvdgd-alnvgsk 473  
 QY 477 DANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNHHIDNVGNARAGIAQAIATAGLVQA 536  
 Db 474 kdnkpvritnvapgvkegdtvnvaqlkgvaqnnnrldnvdgnaragiataglvqa 533  
 QY 537 YLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 594  
 Db 534 ylpkssmmaiggtyrgeagyaigyssisdggnwilkgtasgnsrgrhfgasasvgyqw 591

Search completed: September 5, 2002, 10:23:14  
 Job time: 476 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:19:03 ; Search time 25.63 Seconds  
(without alignments)  
566.087 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKYRIIWSALNAWAVS.....TASGNSRGHFGASASVGQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3019	100.0	594	4	US-09-377-155-9
2	3019	100.0	594	4	US-09-377-155-9
3	2874	95.2	594	4	US-09-377-155-7
4	2874	95.2	594	4	US-09-377-155-7
5	2855	94.6	598	4	US-09-377-155-13
6	2855	94.6	598	4	US-09-377-155-13
7	2852	94.5	598	4	US-09-377-155-5
8	2852	94.5	598	4	US-09-377-155-5
9	2762.5	91.5	599	4	US-09-377-155-15
10	2762.5	91.5	599	4	US-09-377-155-15
11	2758.5	91.4	591	4	US-09-377-155-21
12	2758.5	91.4	591	4	US-09-377-155-21
13	2751	91.1	592	4	US-09-377-155-2
14	2751	91.1	592	4	US-09-377-155-2
15	2739.5	90.7	591	4	US-09-377-155-11
16	2739.5	90.7	591	4	US-09-377-155-11
17	2636	87.3	592	4	US-09-377-155-17
18	2636	87.3	592	4	US-09-377-155-17
19	2616.5	83.4	589	4	US-09-377-155-19
20	2616.5	83.4	589	4	US-09-377-155-19
21	2328.5	44.0	2353	4	US-09-377-155-33
22	2328.5	44.0	2353	4	US-09-377-155-33
23	2328.5	44.0	2353	4	US-09-377-155-33
24	2328.5	44.0	2353	4	US-09-377-155-33
25	2328.5	44.0	2353	4	US-09-377-155-33
26	1261	41.8	607	1	US-08-409-995-6
27	1261	41.8	607	3	US-08-409-995-6

28	1261	41.8	607	4	US-08-913-942-6	Sequence 6, Appli
29	1261	41.8	1912	1	US-08-409-995-4	Sequence 4, Appli
30	1261	41.8	1912	3	US-08-685-467-4	Sequence 4, Appli
31	1055	34.9	1094	4	US-09-268-347-32	Sequence 32, Appli
32	1030	34.1	1098	1	US-08-409-995-2	Sequence 2, Appli
33	1030	34.1	1098	3	US-08-685-467-2	Sequence 2, Appli
34	1030	34.1	1098	4	US-09-377-155-32	Sequence 32, Appli
35	1030	34.1	1098	4	US-08-913-942-2	Sequence 2, Appli
36	1030	34.1	1098	4	US-09-669-974-32	Sequence 32, Appli
37	1030	34.1	1098	4	US-09-268-347-44	Sequence 44, Appli
38	1016	33.7	658	1	US-08-409-995-5	Sequence 5, Appli
39	1016	33.7	658	3	US-08-685-467-5	Sequence 5, Appli
40	1016	33.7	658	4	US-08-913-942-5	Sequence 5, Appli
41	978.5	32.4	679	4	US-08-913-942-15	Sequence 15, Appli
42	978.5	32.4	679	4	US-09-268-347-26	Sequence 26, Appli
43	741	24.5	1004	4	US-09-268-347-30	Sequence 30, Appli
44	727	24.1	1002	4	US-09-268-347-24	Sequence 24, Appli
45	689	22.8	1104	4	US-09-268-347-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match	100.0%	Score 3019;	DB 4;	Length 594;
Best Local Similarity	100.0%;	Pred. No. 1.5e-226;		
Matches 594;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNKYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDLYLE	60	
Db	1	MNKYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDLYLE	60	
QY	61	PVQRTAVVLSRSPKDEGTGEKTEVSDSNWGYVDFKGGVLTAGTITLKAAGNLKIKQNTNE	120	
Db	61	PVQRTAVVLSRSPKDEGTGEKTEVSDSNWGYVDFKGGVLTAGTITLKAAGNLKIKQNTNE	120	
QY	121	NTNASSFTYSLKLDLTDLTSVGTKEKLSFNSANSKNVNTSDTKGLNFAKKTAEINGDTTVH	180	
Db	121	NTNASSFTYSLKLDLTDLTSVGTKEKLSFNSANSKNVNTSDTKGLNFAKKTAEINGDTTVH	180	
QY	181	LNGIGSLTDLTLTGATTNVTNDVDEKKAASVQVNLNAGWNKGVKPGTASDNV	240	
Db	181	LNGIGSLTDLTLTGATTNVTNDVDEKKAASVQVNLNAGWNKGVKPGTASDNV	240	
QY	241	DFVRTYDTVEFLSADTITTTVNVESKDKGKRTVEKIGAKTSVIREKDKGLVTGDKDGEND	300	
Db	241	DFVRTYDTVEFLSADTITTTVNVESKDKGKRTVEKIGAKTSVIREKDKGLVTGDKDGEND	300	
QY	301	SSTDKGEGLVTAKEVIDAVNKGAWRMKMTTANGQTGQADKFPETVTSGTNTVTFASGKGTTA	360	

Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPEFVTSCTNTVTFASGKGTGA 360  
QY 361 TVSKDDQGNITVMYDNNVGDALNVQNLQNSGNWLDKRAVAGSSGKVISGNVSPSKGKME 420  
Db 361 TVSKDDQGNITVMYDNNVGDALNVQNLQNSGNWLDKRAVAGSSGKVISGNVSPSKGKME 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480  
QY 481 PVRITNVAPGVKEGDVTNVAOLKGVQNLNNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRITNVAPGVKEGDVTNVAOLKGVQNLNNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594  
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594

## RESULT 2

US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 100.0%; Score 3019; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred No. 1.5e-226;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNALNANVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWNALNANVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKEVEDSNWGVYFDKGVLTAGITILKAGDNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKEVEDSNWGVYFDKGVLTAGITILKAGDNLIKQNTNE 120  
QY 121 NTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVNITSDTKGLNFAKKTAEFTNGDTTVH 180  
Db 121 NTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVNITSDTKGLNFAKKTAEFTNGDTTVH 180  
QY 181 LNGIGSLTDLTLNLTGATTNVDNVDDEKRAASVKDVLNAGWNIGKVPGCTTASDNV 240  
Db 181 LNGIGSLTDLTLNLTGATTNVDNVDDEKRAASVKDVLNAGWNIGKVPGCTTASDNV 240  
QY 241 DFVRTYDVEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDGKLVTKDKGEND 300  
Db 241 DFVRTYDVEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDGKLVTKDKGEND 300  
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPEFVTSCTNTVTFASGKGTGA 360  
Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPEFVTSCTNTVTFASGKGTGA 360

Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPEFVTSCTNTVTFASGKGTGA 360  
QY 361 TVSKDDQGNITVMYDNNVGDALNVQNLQNSGNWLDKRAVAGSSGKVISGNVSPSKGKME 420  
Db 361 TVSKDDQGNITVMYDNNVGDALNVQNLQNSGNWLDKRAVAGSSGKVISGNVSPSKGKME 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480  
QY 481 PVRITNVAPGVKEGDVTNVAOLKGVQNLNNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRITNVAPGVKEGDVTNVAOLKGVQNLNNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594  
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594

## RESULT 3

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 95.2%; Score 2874; DB 4; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.8e-215;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNALNANVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWNALNANVAVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKEVEDSNWGVYFDKGVLTAGITILKAGDNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKEVEDSNWGVYFDKGVLTAGITILKAGDNLIKQNTNE 120  
QY 121 NTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVNITSDTKGLNFAKKTAEFTNGDTTVH 180  
Db 121 NTNASSFTYSLKKDLTDLTSVTEKLSFGANGKNVNITSDTKGLNFAKKTAEFTNGDTTVH 180  
QY 181 LNGIGSLTDLTLNLTGATTNVDNVDDEKRAASVKDVLNAGWNIGKVPGCTTASDNV 240  
Db 181 LNGIGSLTDLTLNLTGATTNVDNVDDEKRAASVKDVLNAGWNIGKVPGCTTASDNV 240  
QY 241 DFVRTYDVEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDGKLVTKDKGEND 300  
Db 241 DFVRTYDVEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDGKLVTKDKGEND 300  
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPEFVTSCTNTVTFASGKGTGA 360  
Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPEFVTSCTNTVTFASGKGTGA 360  
QY 361 TVSKDDQGNITVMYDNNVGDALNVQNLQNSGNWLDKRAVAGSSGKVISGNVSPSKGKME 420

Db 361 TVSKDDGQNTTVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNNVSPSKGKMD 420  
Qy 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDTNK 480  
Qy 481 PVRTNVPAGVKEGDTVNVAGLKGVAQNLNHHIDNVGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRTNVPAGVKEGDTVNVAGLKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPG 540  
Qy 541 KSMAIAGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 541 KSMAIAGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594

## RESULT 4

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 95.2%; Score 2874; DB 4; Length 594;

Best Local Similarity 95.6%; Pred. No. 2.8e-215;

Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVOASTDDDDLYLE 60  
Db 1 MNKYRIIWNLSALNAWVSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
Qy 61 PVQRTAVVLSFRSDEKGTGEKTEGDSNMWYVFDKRVKAGITLTKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKGTGEKTEGDSNMWYVFDKRVKAGITLTKAGDNLKIKQNTNE 120  
Qy 121 NTNASSFTYSLKDLTDLTSVTEKLSFANSKNVNITSDTKGLNFAKKTAEITNGDTTVH 180  
Db 121 NTNDSFTYSLKDLTDLTSVTEKLSFGANGKNVNITSDTKGLNFAKETAAGTNDPTVH 180  
Qy 181 LNGIGSTLTDLLNTGATTNVDNVDDEKKRAASKVDVLNAGNINIKGVKPGTTASDNV 240  
Db 181 LNGIGSTLTDLLNTGATTNVDNVDDEKKRAASKVDVLNAGNINIKGVKPGTTASDNV 240  
Qy 241 DFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVKEKDGKLVTKGKGEND 300  
Db 241 DFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVKEKDGKLVTKGKGEND 300  
Qy 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKFEVTSGTNVTFASKGTTA 360  
Db 301 SSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKFEVTSGTNVTFASKGTTA 360  
Qy 361 TVSKDDGQNTTVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNNVSPSKGKMD 420

Db 361 TVSKDDGQNTTVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNNVSPSKGKMD 420  
Qy 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDTNK 480  
Qy 481 PVRTNVPAGVKEGDTVNVAGLKGVAQNLNHHIDNVGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRTNVPAGVKEGDTVNVAGLKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPG 540  
Qy 541 KSMAIAGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 541 KSMAIAGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594

## RESULT 5

US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 94.6%; Score 2855; DB 4; Length 598;

Best Local Similarity 94.6%; Pred. No. 8.5e-214;

Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

Qy 1 MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVOASTDDDDLYLE 60  
Db 1 MNKYRIIWNLSALNAWVSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
Qy 61 PVQRTAVVLSFRSDEKGTGEKTEGDSNMWYVFDKRVKAGITLTKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKGTGEKTEGDSNMWYVFDKRVKAGITLTKAGDNLKIKQNTNE 120  
Qy 121 NTNA----SFTYSLKDLTDLTSVTEKLSFANSKNVNITSDTKGLNFAKKTAEITNGD 176  
Db 121 NTNENTDSSFTYSLKDLTDLTSVTEKLSFGANGKNVNITSDTKGLNFAKETAAGTNGD 180  
Qy 177 TVHLNGIGSTLTDLLNTGATTNVDNVDDEKKRAASKVDVLNAGNINIKGVKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATTNVDNVDDEKKRAASKVDVLNAGNINIKGVKPGTTA 240  
Qy 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVKEKDGKLVTKGDK 296  
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVKEKDGKLVTKGDK 300  
Qy 297 GENSSSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKFEVTSGTNVTFASGK 356  
Db 301 DENGSSSTDGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKFEVTSGTKVTFASGN 360  
Qy 357 GTTATVSKDDGQNTTVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNNVSPSKG 416  
Db 361 GTTATVSKDDGQNTTVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNNVSPSKG 420  
Qy 417 KMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSK 476

|||||  
Db 421 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLUSDDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGYAQNLNHNDVGNARAGIAQAATAGLVOA 536  
Db 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGYAQNLNHNDVGNARAGIAQAATAGLVOA 540  
QY 537 YLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 594  
Db 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 598

## RESULT 6

US-09-669-974-13  
; Sequence 13, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 94.6%; Score 2855; DB 4; Length 598;

Best Local Similarity 94.6%; Pred. No. 8.5e-214;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNANVAVSELTNRNHTKRASATVATAVLATLLFAVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNANVAVSELTNRNHTKRASATVATAVLATLLFAVQANATDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKEGTGCEKTEVDSNMGVYFDKGVLTAGTITLKAGDNLKIKONTNE 120  
Db 61 PVORTAVVLSFRSDKEGTGCEKTEVDSNMGVYFDKGVLTAGTITLKAGDNLKIKONTNE 120  
QY 121 NTNA---SSFTYSLKKDLTDLTSVTEKLSFSANSNKVNITSDTKGLNFAKTAETNGD 176  
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKTAETNGD 180  
QY 177 TTVHLNGIGSTLTDLLNTGATTVNTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATTVNTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
QY 237 SDNVDFVRTYDVVEFLUSADTKTTTVNVEKDKGKRTVEVKGAKTSVIKEKDKGLVTGKDK 296  
Db 241 SDNVDFVRTYDVVEFLUSADTKTTTVNVEKDKGKRTVEVKGAKTSVIKEKDKGLVTGKDK 300  
QY 297 GENDSSDDEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVSGTNVTFASGK 356  
Db 301 GENDSSDDEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVSGTNVTFASGK 360  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWNLDSKAVAGSSGKVIISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWNLDSKAVAGSSGKVIISGNVSPSKG 420  
QY 417 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLUSDDEGALNVGSK 476  
|||||

Db 421 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLUSDDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGYAQNLNHNDVGNARAGIAQAATAGLVOA 536  
Db 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGYAQNLNHNDVGNARAGIAQAATAGLVOA 540  
QY 537 YLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 594  
Db 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 598

## RESULT 7

US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 94.5%; Score 2852; DB 4; Length 598;

Best Local Similarity 94.6%; Pred. No. 1.5e-213;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNANVAVSELTNRNHTKRASATVATAVLATLLFAVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNANVAVSELTNRNHTKRASATVATAVLATLLFAVQANATDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKEGTGCEKTEVDSNMGVYFDKGVLTAGTITLKAGDNLKIKONTNE 120  
Db 61 PVORTAVVLSFRSDKEGTGCEKTEVDSNMGVYFDKGVLTAGTITLKAGDNLKIKONTNE 120  
QY 121 NTNA---SSFTYSLKKDLTDLTSVTEKLSFSANSNKVNITSDTKGLNFAKTAETNGD 176  
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKTAETNGD 180  
QY 177 TTVHLNGIGSTLTDLLNTGATTVNTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATTVNTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
QY 237 SDNVDFVRTYDVVEFLUSADTKTTTVNVEKDKGKRTVEVKGAKTSVIKEKDKGLVTGKDK 296  
Db 241 SDNVDFVRTYDVVEFLUSADTKTTTVNVEKDKGKRTVEVKGAKTSVIKEKDKGLVTGKDK 300  
QY 297 GENDSSDDEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVSGTNVTFASGK 356  
Db 301 GENDSSDDEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVSGTNVTFASGK 360  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWNLDSKAVAGSSGKVIISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWNLDSKAVAGSSGKVIISGNVSPSKG 420  
QY 417 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLUSDDEGALNVGSK 476  
Db 421 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLUSDDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGYAQNLNHNDVGNARAGIAQAATAGLVOA 536



|||||  
Db 481 DANKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDVGNARAGIAQAATAGLAQA 540  
QY 537 YLPKGSMAIGGGTYRGAGYAIGYSSISDGGNWTIIKGTASGNSRGHFGASASVGYQW 594  
Db 541 YLPKGSMAIGGGTYRGAGYAIGYSSISDGTGNWVIKGTASGNSRGHFGTSASVGYQW 598  
RESULT 8  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 94.5%; Score 2852; DB 4; Length 598;  
Best Local Similarity 94.6%; Pred. No. 1.5e-213;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
QY 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
Db 1 MNKISRIIWNLSALNAWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEGTEGTEVDSNMWYFDDKKGVLTAAGTITLKGADNLKIKONTNE 120  
Db 61 PVQRTAVVLSFRSDEGTEGTEGDSNMWYFDEKRVLKAGAITLKGADNLKIKONTNE 120  
QY 121 NTNA-----SSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNTSDTKGLNFAKKTAEINGD 176  
Db 121 NTNENTNDSSTYSLKKDLTDLTSVETEKLSTFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
QY 177 TTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240  
QY 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVIEKDGKLVTKGDK 296  
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVIEKDGKLVTKGK 300  
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGOADKFETVTSCTNVTFASG 356  
Db 301 GENGSSDTEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGOADKFETVTSCTVTFASN 360  
QY 357 GTTATVSKDDOGNITVMYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSK 416  
Db 361 GTTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSK 420  
QY 417 KMDETVINAGNNIEITRNGKNIDIATSWTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 421 KMDETVINAGNNIEITRNGKNIDIATSWTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDVGNARAGIAQAATAGLAQA 536  
|||||

Db 481 DANKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDVGNARAGIAQAATAGLAQA 540  
QY 537 YLPKGSMAIGGGTYRGAGYAIGYSSISDGGNWTIIKGTASGNSRGHFGASASVGYQW 594  
Db 541 YLPKGSMAIGGGTYRGAGYAIGYSSISDGTGNWVIKGTASGNSRGHFGTSASVGYQW 598  
RESULT 9  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 91.5%; Score 2762.5; DB 4; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.3e-206;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDLYL 59  
Db 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQANATDEDEEL 60  
QY 60 EPVQRTAVVLSFRSDEGTEGTEVDSNMWYFDDKKGVLTAAGTITLKGADNLKIKQ--- 116  
Db 61 EPVVSALVLOPMIDKEGNESTGNISYIYDHNHTLHGATVTLKAGDNLKIKQNTN 120  
QY 117 -NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNTSDTKGLNFAKKTAEING 175  
Db 121 KNTNENTNDSSTYSLKKDLTDLTSVETEKLSTFGANGKNVNTSDTKGLNFAKETAGTNG 180  
QY 176 DTTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 235  
Db 181 DTTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 240  
QY 236 ASDNVDFVRTYDVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVIEKDGKLVTKGD 295  
Db 241 ASDNVDFVRTYDVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVIEKDGKLVTKG 300  
QY 296 KGENSSDSTDKGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGOADKFETVTSCTNVTFASG 355  
Db 301 KGENSSDTEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGOADKFETVTSCTNVTFASG 360  
QY 356 KGTATVSKDDOGNITVMYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSK 415  
Db 361 KGTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSK 420  
QY 416 KMDETVINAGNNIEITRNGKNIDIATSWTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 475  
Db 421 KMDETVINAGNNIEITRNGKNIDIATSWTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 476 DANKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDVGNARAGIAQAATAGLAQA 535  
Db 481 DANKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDVGNARAGIAQAATAGLAQA 540  
QY 536 AYLPGKSMAIGGGTYRGAGYAIGYSSISDGGNWTIIKGTASGNSRGHFGASASVGYQW 594

```
Db 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 599
|||||
RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E, Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; LENGTH: 599
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 91.5%; Score 2762.5; DB 4; Length 599;
Best Local Similarity 91.7%; Pred. No. 1.3e-206;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MNKIYRIIWNLSALNAWAVAVSELNRHTKRASATVATVATLTLFATVQASTTD-DDDLVL 59
Db 1 MNKIYRIIWNLSALNAWAVAVSELNRHTKRASATVATVATLTLFATVQANATDEDEEL 60
QY 60 EPVQRTAVVLSFRSDKEGTEKEVTEDSNMGVYFDKGVLTAGTITLKAGDNLKIKO--- 116
Db 61 EPVRSALVQFMIDKEGENESTNIGMSIYDHNHTLHAGATVTLKAGDNLKIKONTN 120
QY 117 -NTNENTNASSFTYSLKADLTDLTSVTEKLSFSAANSKNVITSDTKGLNFAKTAETNG 175
Db 121 KWTNENTNDSFTYSLKADLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAETNG 180
QY 176 DTTVHLNGIGSTLTDLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKGVKPGTT 235
Db 181 DTTVHLNGIGSTLTDLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKGVKPGTT 240
QY 236 ASDNVDVRYDYTVFEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDKGLVTGKD 295
Db 241 ASDNVDVRYDYTVFEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDKGLVTGK 300
QY 296 KGENDSSTDKEGGLVTAKEVIDAVNKAAGWRMKTTTTANGOTGOADKFEFVTSNTVTFASG 355
Db 301 KGENDSSTDKEGGLVTAKEVIDAVNKAAGWRMKTTTTANGOTGOADKFEFVTSNTVTFASG 360
QY 356 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 415
Db 361 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 420
QY 416 GKMDVTNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475
Db 421 GKMDVTNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480
QY 476 KDANKPVRTNVPACVKEGDTVNVQALKGVQAOVLNHNHIDVGNARAGIAQATAGLVQ 535
Db 481 KDANKPVRTNVPACVKEGDTVNVQALKGVQAOVLNHNHIDVGNARAGIAQATAGLVQ 540
QY 536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 594
|||||
```

```
Db 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 599
|||||
RESULT 11
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E, Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; TYPE: PRT
; LENGTH: 591
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 91.4%; Score 2758.5; DB 4; Length 591;
Best Local Similarity 92.3%; Pred. No. 2.6e-206;
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWAVAVSELNRHTKRASATVATVATLTLFATVQASTTD---DDDL 57
Db 1 MNKIYRIIWNLSALNAWAVAVSELNRHTKRASATVATVATLTLFATVQASANNEEQEEDL 60
QY 58 YLEPQRTAVVLSFRSDKEGTEKE--VTEDSNMGVYFDKGVLTAGTITLKAGDNLKIKO 116
Db 61 YLDPQRTAVVLIYNSDKEGTEKEKEVENSQWYFNEKGVLTARETITLKAGDNLKIKO 120
QY 117 -NTNENTNASSFTYSLKADLTDLTSVTEKLSFSAANSKNVITSDTKGLNFAKTAETNGD 176
Db 121 -----NCTNFTYSLKADLTDLTSVTEKLSFSAANSKNVITSDTKGLNFAKETAETNGD 174
QY 177 TTVHLNGIGSTLTDLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
Db 175 TTVHLNGIGSTLTDLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKGVKPGTTA 234
QY 237 SDNVDVRYDYTVFEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDKGLVTGDK 296
Db 235 SDNVDVRYDYTVFEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDKGLVTGDK 294
QY 297 GENDSSTDKEGGLVTAKEVIDAVNKAAGWRMKTTTTANGOTGOADKFEFVTSNTVTFASG 356
Db 295 GENDSSTDKEGGLVTAKEVIDAVNKAAGWRMKTTTTANGOTGOADKFEFVTSNTVTFASG 354
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 416
Db 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 414
QY 417 KMDVTNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 415 KMDVTNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
QY 477 DANKEPVRTNVPACVKEGDTVNVQALKGVQAOVLNHNHIDVGNARAGIAQATAGLVQ 536
Db 474 KDNKEPVRTNVPACVKEGDTVNVQALKGVQAOVLNHNHIDVGNARAGIAQATAGLVQ 533
QY 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 594
Db 534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 591
|||||
```

## RESULT 12

US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6331173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 91.4%; Score 2758.5; DB 4; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2.6e-206;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
  
Qy 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTD---DDDL 57  
Db 1 MNKIYRIWNSALNAWVSVSELTRNHTKRASATVKVATVATLTLFATVQASNEEQEDL 60  
  
Qy 58 YLEPVQRTAVVLSFRSDEKGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIK 116  
Db 61 YLDPVQRTAVVLIYNSDEKGTGEKEVENSQWAVYFNEKGVLTAREITLKAGDNLKIK 120  
  
Qy 117 NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKTAETNGD 176  
Db 121 -----NGTFTYSLKKDLTDLTSVGTSEKLSFSAANGKNVNTSDTKGLNFAKTAETNGD 174  
  
Qy 177 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVKPGTTA 236  
Db 175 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVKPGTTA 234  
  
Qy 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVKEKDGKLVTKGD 296  
Db 235 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVKEKDGKLVTKGD 294  
  
Qy 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFETVTSCTNVTFSAGK 356  
Db 295 GENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFETVTSCTNVTFSAGK 354  
  
Qy 357 GTTATVSKDDQGNITVMYDYNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSK 416  
Db 355 GTTATVSKDDQGNITVMYDYNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSK 414  
  
Qy 417 KMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDDEGALNVGSK 476  
Db 415 KMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473  
  
Qy 477 DANKPVRITNVAPGVKEGDTVNAQLKGAQNLANHNDVGNARAGTAAQAIATAGLVQA 536  
Db 474 KDNKPVRIITNVAPGVKEGDTVNAQLKGAQNLANHNDVGNARAGTAAQAIATAGLVQA 533  
  
Qy 537 YLPKSMMAIGGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594  
Db 534 YLPKSMMAIGGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

## RESULT 13

RESULT 14  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6331173

US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 91.1%; Score 2751; DB 4; Length 592;  
Best Local Similarity 92.0%; Pred. No. 1e-205;  
Matches 551; Conservative 13; Mismatches 23; Indels 12; Gaps 4;  
  
Qy 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTDD----DD 56  
Db 1 MNKIYRIWNSALNAWVSVSELTRNHTKRASATVKVATVATLTLFATVQASANNRPKRD 60  
  
Qy 57 YLEPVQRTAVVLSFRSDEKGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIK 115  
Db 61 YLDPVQRTAVVLIYNSDEKGTGEKEVENSQWAVYFNEKGVLTAREITLKAGDNLKIK 120  
  
Qy 116 QNTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKTAETNG 175  
Db 121 Q-----NGTFTYSLKKDLTDLTSVGTSEKLSFSAANGKNVNTSDTKGLNFAKTAETNG 174  
  
Qy 176 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVKPGTT 235  
Db 175 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVKPGTT 234  
  
Qy 236 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVKEKDGKLVTKGD 295  
Db 235 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVKEKDGKLVTKGD 294  
  
Qy 296 KGENDSSTDKEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFETVTSCTNVTFSAG 355  
Db 295 KGENSSDDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFETVTSCTNVTFSAG 354  
  
Qy 356 KGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSK 415  
Db 355 KGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSK 414  
  
Qy 416 GKMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDDEGALNVGSK 475  
Db 415 GKMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473  
  
Qy 476 KDANKPVRITNVAPGVKEGDTVNAQLKGAQNLANHNDVGNARAGTAAQAIATAGLVQ 535  
Db 474 KDNKPVRIITNVAPGVKEGDTVNAQLKGAQNLANHNDVGNARAGTAAQAIATAGLVQ 533  
  
Qy 536 AYLPKSMMAIGGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594  
Db 534 AYLPKSMMAIGGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592

```
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2
```

```
Query Match 91.1%; Score 2751; DB 4; Length 592;
Best Local Similarity 92.0%; Pred. No. 1e-205;
Matches 551; Conservative 13; Mismatches 23; Indels 12; Gaps 4;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD---DD 56
DB 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQASANNRPKDD 60
QY 57 LYLEPQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIK 115
DB 61 LYLDPQRTAVVLSFRSDKEGTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 116 QNTNENTNASSFTYSLKDKLDTLTSVGTSEKLSFNSANKVNITSDTKGLNFAKKTAEITNG 175
DB 121 Q-----NGTFTYSLKDKLDTLTSVGTSEKLSFNSANGKNVITSDTKGLNFAKKTAEITNG 174
QY 176 DTTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTT 235
DB 175 DTTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTT 234
QY 236 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDKGRTEVKIGAKTSVIEKDKGLVTGKD 295
DB 235 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDKGRKTEVKIGAKTSVIEKDKGLVTGKD 294
QY 296 KGENSDTDKEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEVTSCTNVTFSAG 355
DB 295 KGENSDTDEGELVTAKEVIDAVNKAQRMTTANGOTGOADKFEVTSCTNVTFSAG 354
QY 356 GTTATVSKDDQGNITVMDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSK 415
DB 355 GTTATVSKDDQGNITVMDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSK 414
QY 416 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475
DB 415 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 473
QY 476 KDANKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAATATAGLVQ 535
DB 474 KDNKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAATATAGLVQ 533
QY 536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 594
DB 534 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 592
```

```
RESULT 15
US-09-377-155-11
; Sequence 11, Application US/093771155
; Patent No. 6197312
; GENERAL INFORMATION:
```

```
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11
```

```
Query Match 90.7%; Score 2739.5; DB 4; Length 591;
Best Local Similarity 91.8%; Pred. No. 7.9e-205;
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD---DDD 57
DB 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQASANNRQEDDL 60
QY 58 LYLEPQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIK 116
DB 61 LYLDPVLRVAVLVISNDSKDEGTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 117 NTNENTNASSFTYSLKDKLDTLTSVGTSEKLSFNSANKVNITSDTKGLNFAKKTAEITNG 176
DB 121 -----NGTFTYSLKDKLDTLTSVGTSEKLSFNSANGKNVITSDTKGLNFAKKTAEITNG 174
QY 177 TTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTTA 236
DB 175 TTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTTA 234
QY 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDKGRTEVKIGAKTSVIEKDKGLVTGDK 296
DB 235 SDNVDFVRTYDVEFLSADTKTTTVNVESKDKGRKTEVKIGAKTSVIEKDKGLVTGDK 294
QY 297 KGENSDTDKEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEVTSCTNVTFSAG 356
DB 295 KGENSDTDEGELVTAKEVIDAVNKAQRMTTANGOTGOADKFEVTSCTNVTFSAG 354
QY 357 GTTATVSKDDQGNITVMDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSK 416
DB 355 GTTATVSKDDQGNITVMDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSK 414
QY 417 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 476
DB 415 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 473
QY 477 KDANKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAATATAGLVQ 536
DB 474 KDNKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAATATAGLVQ 533
QY 537 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 594
DB 534 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 591
```

Search completed: September 5, 2002, 10:23:46  
Job time: 263 sec

---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:20:33 ; Search time 34.15 seconds  
(without alignments)  
1671.364 Million cell updates/sec

Title: US-09-700-293-2

Perfect score: 3019

Sequence: 1 MNKYRIIWSALNAWAVS.....TASGNSRGHFGASASGVQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2758.5	91.4	591	2 G81133	adhesin NMB0992 [i
2	2533	83.9	592	2 A81888	probable surface f
3	620	20.5	298	2 I64138	adhesin homolog HI
4	398.5	13.2	2059	2 D82671	surface protein XF
5	384.5	12.7	1190	2 AC2615	probable autotrans
6	375.5	12.4	1107	2 AC0976	probable adhesin Z
7	368.5	12.2	1388	2 A86036	probable adhesin E
8	368.5	12.2	1588	2 H91188	probable adhesin p
9	331.5	11.0	658	2 AH0110	probable surface p
10	244	8.1	1091	2 G64964	hypothetical prote
11	239	7.9	1004	2 C82672	surface-exposed ou
12	224	7.4	2249	2 A41477	190K surface antig
13	222	7.4	1018	2 H83135	probable adhesin p
14	220	7.3	1536	2 A43855	high-molecular-we
15	219	7.3	1286	2 S28634	adhesin AIDA-I pre
16	219	7.3	4919	2 T31105	hypothetical prote
17	216.5	7.2	1325	2 A64905	ydek protein - Esc
18	216	7.2	1487	2 AG2560	hypothetical prote
19	214.5	7.1	949	2 D90803	Aida-I adhesin-lik
20	214.5	7.1	1005	2 H85611	probable adhesin Z
21	213	7.1	3705	2 AD0123	probable autotrans
22	211.5	7.0	1477	2 B43855	high-molecular-we
23	209.5	6.9	1910	2 AF0394	probable adhesin h
24	209	6.9	5188	2 B85547	probable RTX famil
25	209	6.9	5291	2 F90696	hypothetical prote
26	208	6.9	1327	2 B90674	Aida-I adhesin-lik
27	208	6.9	1349	2 E85524	probable beta-barr
28	205.5	6.8	936	2 I40711	sapB protein - Cam
29	204.5	6.8	1577	2 A35140	hemolysin A precu

30	203.5	6.7	1343	2 D85724	hypothetical prote
31	203	6.7	1608	2 A28182	hemolysin A - Serr
32	203	6.7	4936	2 AH2515	hypothetical prote
33	201.5	6.7	1109	2 A56143	surface-array prot
34	200.5	6.6	1343	2 E90893	hypothetical prote
35	200	6.6	980	2 H90681	probable flagellin
36	200	6.6	980	2 D85532	probable structur
37	200	6.6	3013	2 AB0480	probable invasin Y
38	198	6.6	2020	2 C48399	ABC-type transport
39	197	6.5	2551	2 B98047	hypothetical prote
40	197	6.5	3029	2 S76109	hypothetical prote
41	195	6.5	1029	2 T30852	outer membrane pro
42	195	6.5	1417	2 A83080	hypothetical prote
43	194.5	6.4	4152	2 T31102	filamentous hemag
44	194	6.4	920	2 I40614	surface array prot
45	194	6.4	2468	2 A83412	hypothetical prote

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC38 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Accession: G81133

R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <FET>

A:Cross-references: GB:AE002450; GB:AE002098; MID:g7226229; PIDN:AAF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 91.4%; Score 2758.5; DB 2; Length 591;

Best Local Similarity 92.3%; Pred. No. 1.5e-131;

Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

QY 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDD 57

Db 1 MNKYRIIWSALNAWVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEDL 60

QY 58 YLPVQRTAVVLFPSRDSKEGTGEKE-VTEDSNGVYEDKKGVLTAGTITLKAQGNLKIKQ 116

Db 61 YLPVQRTAVVLFVNSDKGTGEKEKVEENSQWAVYENKGVLTAREITLKAQGNLKIKQ 120

QY 117 NTNENTNASSFTYSLKKDLTLDSVGTGKLSFSANSNKVNTSDTKGLNFAKTAETNGD 176

Db 121 -----NGTFTYSLKKDLTLDSVGTGKLSFSANGKNVNTSDTKGLNFAKTAETNGD 174

QY 177 TTVHLNGIGSTLTDTLTNGTATTNTNDVTDDEKRAASVKDVLNAGWNIKGVPQTGA 236

Db 175 TTVHLNGIGSTLTDTLTNGTATTNTNDVTDDEKRAASVKDVLNAGWNIKGVPQTGA 234

QY 237 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTVKIGAKTSVKEKDKLVTKGDK 296

Db 235 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTVKIGAKTSVKEKDKLVTKGDK 294

QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGAADKFFVTSGTNNVTFSAGK 356

Db 295 GENDSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGAADKFFVTSGTNNVTFSAGK 354

QY 357 GTTATVSKDQGNITVNYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416

Db 355 GTTATYKDDQGNITVMDVNVGDALNVQLNSGWNLDKAVAGSSKVIISGNVSPKG 414  
Qy 417 KMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 415 KMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473  
Qy 477 DANKPVRIITNAPGKEDGVTNVAQLKGVAQNLNHIDNVGNARAGIAQAIAATAGLVQA 536  
Db 474 KDNKPVRIITNAPGKEDGVTNVAQLKGVAQNLNHIDNVGNARAGIAQAIAATAGLVQA 533  
Qy 537 YLPKSNMAIGGGTGRGAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGYOW 594  
Db 534 YLPKSNMAIGGGTGRGAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGYOW 591

RESULT 2  
A:1888  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
Holroyd, S.; Jagsals, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000.  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain Z2491  
A:Genetics:  
A:Gene: NMA1200

Query Match 83.98; Score 2533; DB 2; Length 592;  
Best Local Similarity 86.48; Pred. No. 3.2e-120;  
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;

Qy 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD-DDDLXL 59  
Db 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60  
Qy 60 EPVORTAVVLSFRDKGTGEKE-----VTEDSNMGVYFDKKGVLTAGTITLKAGDNLKI 114  
Db 61 ESVOR-SVVGSIQASMEGSELETISLSMTDS-----KEFVDPYIVVTLKAGDNLKI 112  
Qy 115 KONTNENTNASSFTYSLAKDLTDLTSVGTGKLSFANSKNVITSDTKGLNFAKKTAEIN 174  
Db 113 KONTNENTNASSFTYSLAKDLTGLINVTETKLSFGANGKVVLIISDTKGLNFAKKTAEIN 172  
Qy 175 GDTTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGNIIKGVKPGT 234  
Db 173 GDTTVHLNGIGSTLTDLLAGSASHVDAGNQST--HYTRAASIKDVLNAGNIIKGVKPGT 230  
Qy 235 TA--SONVDFVRYTVTFELFADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVT 292  
Db 231 TTQSENDFVRYTVTFELFADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVT 290  
Qy 293 GKDKGENDSSTDKGELVTAKEVIDAVNKGWRMKTITANGQTGOADKPFETVTSGTNVTF 352  
Db 291 GKDKGENDSSTDEGELVTAKEVIDAVNKGWRMKTITANGQTGOADKPFETVTSGTNVTF 350  
Qy 353 ASKGGTATVSVKDDQGNITVMDVNVGDALNVQLNSGWNLDKAVAGSSKVIISGNVS 412  
Db 351 ASKGGTATVSVKDDQGNITVMDVNVGDALNVQLNSGWNLDKAVAGSSKVIISGNVS 410  
Qy 413 PSKGMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDVDEGALN 472  
Db 411 PSKGMDETVINAGNIEITRNKNIDIAISMTQFSSVSLGAGADAPTLSDVDEGALN 470

Qy 473 VGSKDANKPVRIITNAPGKEDGVTNVAQLKGVAQNLNHIDNVGNARAGIAQAIAATAG 532  
Db 471 VGSKDANKPVRIITNAPGKEDGVTNVAQLKGVAQNLNHIDNVGNARAGIAQAIAATAG 530  
Qy 533 LVQAYLPGKSNMAIGGGTGRGAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGY 592  
Db 531 LVQAYLPGKSNMAIGGGTGRGAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGY 590  
Qy 593 QW 594  
Db 591 QW 592

RESULT 3  
I64138  
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: I64138  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
D.M.; Branno, R.C.; Faye, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995.  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:gl574588; PID:gl574589; TIGR:HI1732

Query Match 20.5%; Score 620; DB 2; Length 298;  
Best Local Similarity 46.6%; Pred. No. 2e-24;  
Matches 145; Conservative 41; Mismatches 91; Indels 34; Gaps 7;

Qy 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD-DDDLXL 60  
Db 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD-DDDLXL 60  
Qy 61 PVORTAVVLSFRDKGTGEKEVTEDSNMGVYFDKKGVLTAG-TITLKAGDNLKIKONTN 119  
Db 50 -INDAGTFVVKVQSTEDDIEDSAATKDDN-----KNQALKAGDTLTLKAGNKLAKL--- 99  
Qy 120 ENTNASSFTYSLAKDLTDLTSVGTGKLSFANS-----SNKNVITSDTKGLNFAKKTAE 172  
Db 100 -DOGKSVTFALAKDLDTAKVSDTLTIGNTPAAGGATPKVSTITADGLKLAK---G 155  
Qy 173 TNGDTTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGNIIKGVK 232  
Db 156 TNGDTTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGNIIKGVK 214  
Qy 233 GTTASNDVFRYTVTFELFADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVT 292  
Db 215 AGNTENVDLVAGYDNVEITGDKNTLDVLTAKENGKTEVKFTPKTSVINKDNKLLT 274  
Qy 293 GKDKGENDSST 303  
Db 275 GKOLKANTGT 285

RESULT 4

D82671  
surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below





```
Db 1003 F-----VKVNSLNN-----SATPLAACGVDATAIGVCATASGADSI 1037
QY 461 -----PTLSVDDEGAL-----NVGSKDANKPVRIINAVPGVKEGDVTVNAOLK 503
Db 1038 AMGNKASADNAVAIGHNSVADRANTVSVGSAGSER--QVTNVAAGTADTDAVNVSQLN 1095
QY 504 GVAQNLNNHIDVNGNAR---AGIAQAIATAGLVQAYLPGRKSMIAIGGGYRGEAGYAI 559
Db 1096 QGLITAKQVTDGVVGSRLRRDGDGVAATATANLPOAVTPGRMTSVGVSSYRGSIAIV 1155
QY 560 GYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 594
Db 1156 GVSSVSGRWFVFKFSGSANTRSQVIGAGVGYQW 1190

RESULT 6
AC0976
Probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.;
  Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.;
  Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
  et al.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
  Typhimurium
A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:gl6504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 12.4%; Score 375.5; DB 2; Length 1107;
Best Local Similarity 21.7%; Pred. No. 2.4e-11;
Matches 189; Conservative 105; Mismatches 262; Indels 299; Gaps 33;

QY 27 TKRASATVAVATLTLFATVQASTD---DDLY---LEPQVAVVLSFRSKEGTGE 80
Db 273 TFSASRNGASKITNLAAGTLASIDAVNGSQLFETNQKVDQNTSAIADINTSITLSS 332
QY 81 KEVTEDSNWGVYFDKKGVLTAGTIT--LKAGD-----NLKIKQNT--- 118
Db 333 DNLQWNETTNSFSASGSGSTTKIINVAAGELSEESTDAVNGSQLFETNEKVDQNTDIA 392
QY 119 -----NENTNASSFTYSLKKDLTDLTSVGTGL--SFSAN--SNKVNITSDT 161
Db 393 ANTNIQNTQNTAENLNTSVSDINTSI--TGLTDNALWDEDTCFASNHGSGTSKITNVA 451
QY 162 KGLNFAKKTAEFTG---DTHVHLNGISGLTDLTLTGATTVNNDVTDDEKRAASV 217
Db 452 AGALSEDSTDAVNGSQLFETNQKVDQNTSAIAD--INT--SITNLGTDALSDDEEGAFSA 508
QY 218 KDVNLAGWNILKGVKPTASDNVDFV---RYDFT-----VEFLSADTKTTVN-- 262
Db 509 SHGTSQNTKTNVAAGEIASDSDAINGSQLFETNMLISQYNESISQLAGDFTSEYITEN 568
QY 263 -----VESKDNGKRTVEKIGAKTSVIEKDGKLVTKDK--RYDFT-----GENDSSTDKG 306
Db 569 GTGVKVIKRTNDNGLEGQ-----DAYATNGATVGVDAVAGGACCLALGONSSSTEG 621
QY 307 -----EGLV-----TAKEVIDAVNKA---GWRKKTWTAN 332
Db 622 SIALGSGSTSNRAITTGIRETSATSDGVVIGYNTDRELLGALSGLTGDSYRQITNVAD 681
QY 333 GQTGQ-----ADKPEVTISGNTVTFASGKGTW-----TVSKDDOG-- 368
Db 682 GSEAQDAVTVROLQNAIGAVTTTPTKYYHANSTEEDSLAVGTDLSLMAKAKTIVNADAGIG 741
```

```
QY 369 ---NITVWTDVNVGDALNVN-----QLONGWNLDSK----- 397
Db 742 IGLNTLVMAADALNGAIGSNARHANHSIAMNGSOTTTRAQDTAYTNMDTPQNSVGEF 801
QY 398 AVAGSGKVISGNSPSPKGMDETIVTNAG---NNIEITRNGKNI----- 439
Db 802 SVGSEDDGQRIITNVAAGSADTDA---VNVGQLKVTDQAVSRNTQSITNLNTQVSNLDTRV 858
QY 440 ---DIATSMTPQF-----SSVSLGAGADAP-----TSLVDDE 468
Db 859 TNIENGIGDIVTGTSTKFKFTNTDGDANAGQASVAIGSGSIAAAENSVALGTNSVADE 918
QY 469 -GALNVGSKDANKPVRIINAVPGVKEGDVTVNAQLK----- 503
Db 919 ANTVSVGSSTQOR--RIINVAAGVNNNTDAVNAQLKASEAGSVRYETNADGSMVNSVLNL 976
QY 504 -----GVAQ-----NLNNHIDNVNDCNARAG 523
Db 977 GDSGCGTTRIGNVSAAVNDTDVAVYQLKRSVEEANTYTDQKMGEMNSKIKGIENKMSG 1036
QY 524 IQAQTATAGLVQAYLPGRKSMIAIGGGYRGEAGYAISSIDGNNWIIKGTASGNSRGRH 583
Db 1037 IASAMAGLPOATAPANNMISTAGGTFNGESAVALGVSMVSESGWVYKLGQTSNSQGD 1096
QY 584 FGASASVGYQW 594
Db 1097 YSAIIGAGFQW 1107

RESULT 7
AB6036
Probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: AB6036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
  Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoculis, K.; Apoda
  Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: AB6036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; NID:gl2518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
  A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5029

Query Match 12.2%; Score 368.5; DB 2; Length 1588;
Best Local Similarity 23.0%; Pred. No. 7.4e-11;
Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;

QY 7 IIV-----NSALNANVAVSELTRNHTKRASATVATATLTLFATVQASTTDDDDLYLE 60
Db 880 LLMDADAGENGAFSA-----AHGKDKTASVITNV-ANGAISAASSDAINGSQLY-- 927
QY 61 PVQRTAVVLSFRSKEGTGEKTEVDSNMGVYFDKKGVLTAGTITL-----KAGDNLKI 114
Db 928 -----TTNKYIADALG-GDAEVNAD-----GTITAPTYYTIANAEYNNVGDALDA 970
QY 115 KQNT-----NENTNASSFTY-----SLKKDLTDL---TSVGTGLKLSFSA 150
Db 971 LDNALLMDETANGGAGAYNASHDGKASIITNVANGSISDSDTDAVNGSQLNATNMIEQ 1030
QY 151 NSKNVN-----ITSPTKGLNFAKKTAEFTGNTTTHLNGI----- 184
Db 1031 NTOIINOLAGNTDATYIENGAGINRYRTNDGDLAFNDASAOQGVGATAGYNSVAKGDS 1090
QY 185 -----GSTLTDTLLNTGA-TTNVTNNDNV-----TDEKKAASVKD 219
Db 185 -----GSTLTDTLLNTGA-TTNVTNNDNV-----TDEKKAASVKD 219
```

Db 1091 VAIGQSYSDVDTGIALGSSVSSRVIAKGRSDTSTENGWVIGYDTTDELLGALSIGD 1150  
QY 220 -----VLNAGWNIKGKPGTTASDNVDFRVYDTVEFLSADTKTTTNNVESKDNGK--- 270  
Db 1151 DCKYROIIN-----VADGSEAHDAVT-VROLQAIGAVALTPTKYFHFANSTEEDSLAV 1202  
QY 271 -RTEVKIGAKTSVIKPK-----DGKLVTKGDKGEND-----SSTDKGEGLVTAKE 314  
Db 1203 GTDSLAMGAKTIVNGDKGIGIGYGAVVDANALNGIAIGSNAQVIHNSIAIGNSTTTRG 1262  
QY 315 V-----IDAVNKAGWRMKTITANGO-----TGQADKPEFTVSCGNTVTFASCKGTT 359  
Db 1263 AQTNYTAYNDAPQNSVGFSGSADGQROITNVAAGSAD-----TDAVNV--GOLKVTD 1315  
QY 360 ATYSKDDQGNITVM-----YDVNVGDAL-----NVNQLQNSGWNLDS 396  
Db 1316 AQVSQNTQ-SITNLDNRVTNLDNRVTNIENGIDIVTTGSTKYFKTNTDGVDAQAOKDS 1374  
QY 397 KAVAGSSGKVISGNVSPSKGM---DETNNINAGNNIEITRN---GKNIDIAIATSMPTQFS 450  
Db 1375 VAIGSGSIAAADNSVALGTGCVATEENTISVGSSTNORRITNVAAGKNATDAVNVQAOLKS 1434  
QY 451 SVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQ--- 507  
Db 1435 SEAGGVRYDTKADGSDYSNITLGGGNGG-TTRISNVSAVNNNDVYNTVAQLKQSVQETK 1493  
QY 508 -----NLNNHIDNVNAGARAGIAQAATAGLVQAYLPGKSMMAIGGTYRGEAGYAI 559  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGSIASAMATGLPOAYTPGASMASIGGTYNGESAVAL 1553  
QY 560 GYSSISDGGNWIITGTASNSRHFSGASVGYQW 594  
Db 1554 GVSWSANGRWVYKLGQSTNSQGEYSAAALGAGIQW 1588  
  
RESULT 8  
H91188  
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A:Reference number: A99629; PMID:11256796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs4480.  
  
Query Match 12.2%; Score 368.5; DB 2; Length 1588;  
Best Local Similarity 23.0%; Pred. No. 7.4e-11;  
Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;  
  
QY 7 IIW-----NSALNAWVASELNRHTRKRASATVATAVATLFLATVQASTTDDDDLYLE 60  
Db 880 LLWDADAGAGAFSA-----AHGKDKTASVITNV-ANGAISAASSDAINGSQLY-- 927  
QY 61 PVQRTAVVLSFRSDKRGTEKEVETDSNWGVYFDKGVLTAGTITL-----KAGNLKI 114  
Db 928 -----TTNKYIADALG-GDAEVNAD-----GTITAPTYITIANAEYNNVNGDALDA 970  
QY 115 KONT-----NENTNASSFTY-----SLKKDLTDL---TSVGTEKLSFSA 150  
Db 971 LDNALWDETANGGAGAYNASHDGKASITNVANGISIEDSTDAVNGSOLNATNMWIEQ 1030  
QY 151 NSKNVN-----ITSDTKGLNFAKKTAEETNGDVTTHLNGI----- 184

Db 1031 NTQIIINQLAGNTDATYIQENGAGINVTNRNDGLAFENDASQGVGATAIGYNSVAKGDSS 1090  
QY 185 -----GSTLDTLLNTCA-TTNTVNDNV-----TDEKKRAASVDK 219  
Db 1091 VAIGQSYSDVDTGIALGSSVSSRVIAKGRSDTSTENGWVIGYDTTDELLGALSIGD 1150  
QY 220 -----VLNAGWNIKGKPGTTASDNVDFRVYDTVEFLSADTKTTTNNVESKDNGK--- 270  
Db 1151 DCKYROIIN-----VADGSEAHDAVT-VROLQAIGAVALTPTKYFHFANSTEEDSLAV 1202  
QY 271 -RTEVKIGAKTSVIKPK-----DGKLVTKGDKGEND-----SSTDKGEGLVTAKE 314  
Db 1203 GTDSLAMGAKTIVNGDKGIGIGYGAVVDANALNGIAIGSNAQVIHNSIAIGNSTTTRG 1262  
QY 315 V-----IDAVNKAGWRMKTITANGO-----TGQADKPEFTVSCGNTVTFASCKGTT 359  
Db 1263 AQTNYTAYNDAPQNSVGFSGSADGQROITNVAAGSAD-----TDAVNV--GOLKVTD 1315  
QY 360 ATYSKDDQGNITVM-----YDVNVGDAL-----NVNQLQNSGWNLDS 396  
Db 1316 AQVSQNTQ-SITNLDNRVTNLDNRVTNIENGIDIVTTGSTKYFKTNTDGVDAQAOKDS 1374  
QY 397 KAVAGSSGKVISGNVSPSKGM---DETNNINAGNNIEITRN---GKNIDIAIATSMPTQFS 450  
Db 1375 VAIGSGSIAAADNSVALGTGCVATEENTISVGSSTNORRITNVAAGKNATDAVNVQAOLKS 1434  
QY 451 SVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQ--- 507  
Db 1435 SEAGGVRYDTKADGSDYSNITLGGGNGG-TTRISNVSAVNNNDVYNTVAQLKQSVQETK 1493  
QY 508 -----NLNNHIDNVNAGARAGIAQAATAGLVQAYLPGKSMMAIGGTYRGEAGYAI 559  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGSIASAMATGLPOAYTPGASMASIGGTYNGESAVAL 1553  
QY 560 GYSSISDGGNWIITGTASNSRHFSGASVGYQW 594  
Db 1554 GVSWSANGRWVYKLGQSTNSQGEYSAAALGAGIQW 1588  
  
RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [Imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; PMID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902  
  
Query Match 11.0%; Score 331.5; DB 2; Length 658;  
Best Local Similarity 25.0%; Pred. No. 1.7e-09;  
Matches 132; Conservative 73; Mismatches 209; Indels 113; Gaps 21;  
  
QY 99 LTAGTITLAKGDNLTKQNTNENTNASSFTYSLKKDLTDLTSVGTKEKLSFSAANSKVNIT 158  
Db 214 LGAGAVTSQA--NSIALGAASINTVGAQSSYSAYALTAPQASVGGELGIGTALGNRKIT-- 269  
QY 159 SDTKGLNFAKKTAEETNGDVTTHLNGIGSTLTDLLNTGATTNVTN--DNVTDDEKRAAS 216  
Db 270 -----GVAAGSASSDAVNVQAQLTAVGDQVQON-----TANITSLGGRVTITIE----GS 313

QY 217 VKDVLNAGNLIKGVKPGTTASDNVDFRTYDVEFLSADTKTTTVNVESKNGKRT---- 272  
Db 314 MASIANGG-GVYFPHANSTPDV-----ASGTSVAIGFASLAAALASG 360  
QY 273 --EYKIGAKTSVIEKDKGLVTCCKDGENSDSTDKGEGLVTAKEVIDAVNKAGWRKTTT 330  
Db 361 AGAVAIG--DGAASADGSAVIGCGSDN-----GRGV---ENWICKYSNA-----SMT 404  
QY 331 ANGOTQADKFEETVTSCTNVTTFASGKGTATVSKDDQGNITVMTVDVNVGDALNVQLQNS 390  
Db 405 SSG-----TVSGNGTAT-----GETRTVSNVADG-----LQATDAVNLRLDQ- 442  
QY 391 GWNLDKAVAGSSKGVISGNVSPSKGMDETYNINAGNNI-EITRNGKNIDI--ATSMTP 447  
Db 443 -----IAASTVYVYNNVSGLQGTDMFQVNNSSGLAKPSATGANSATGGAGSVAS 493  
QY 448 QFSSVSLGADAPTL-----VDDGALNVGSKDANKPVRIITNVAPGVKEGDVTN 498  
Db 494 GNNSTAFGSGAKATAANSAAALGANSVADRANSVSGVSGNER--QITNVAPATQGTDAVN 551  
QY 499 VAQLKGVAQNLNNHIDNVGNAR-----AGIAQALATAGLVOAYLPCKSMMAIG 547  
Db 552 FDLKSIISQTNATNYRSELKODLRKONSLSAGIASAMSLTOPVTSGSSMTTIG 611  
QY 548 GGTGREGAGYAGVSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594  
Db 612 AASYRGQSALSLGVSSISDSGRVWSKLQASSNTQDGFIGVGVGYOW 658

## RESULT 10

G64964  
Hypothetical protein b2000 - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Feb-2001  
C:Accession: G64964  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
S:Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: G64964  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1091 <BLAT>  
A:CROSS-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g1788309;  
A:Experimental source: strain K-12, substrain MG1655  
C:Keywords: nucleotide binding; P-loop  
F:683-690/Region: nucleotide-binding motif A (P-loop)

Query Match 8.1%; Score 244; DB 2; Length 1091;  
Best Local Similarity 22.6%; Pred. No. 8.3e-05;  
Matches 141; Conservative 64; Mismatches 215; Indels 204; Gaps 28;  
QY 1 MNKYRIIWSNALNAWAVSELTRNHTKRASATVATVATLFLFATVQASTDDDDLYLE 60  
Db 57 LNTCYRLVNNHMTGAVASELARARGGVAVALSAAVTSPLVLA-----DIVVH 110  
QY 61 PVORTAVVLSFRSDKEGTGEKTEVDNSNGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
Db 111 P-----GE-----TVNGGTLANHDNQIVFTTNG 134  
QY 121 WTNASSFTYSLKDLTDLISVTEKLSFSAANSKNVITSDTKGLNFAKKTAEETNGTTHV 180  
Db 135 MTISGLEIGPDNE-----ANTGGQWQDGGTANKTTVTSG--GLQRVNPGGSVS-DTVIS 187  
QY 181 LINGIGSTL-----TDTLLNTG-----ATTNVTNDVNDDEKKAASVKVLYNAGWI 227  
Db 188 AGG-GQSQQGAVNTTNGEQQMHGAIATGTVINDK-----GWQV 228  
QY 228 KGVKPGTASDNVDFRT-----YDIVEFLSADTKTTTVNVESKNGKRTVKIG 277  
Db 229 --VRPGTATDTV--VNTGAEGGPDANGDTGQFVRGDAVRTTN-----KNGRQIVRABG 280

## RESULT 11

C82672  
Surface-exposed outer membrane protein XFI516 [imported] - Xylella fastidiosa (strain  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: C82672  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: C82672  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A:CROSS-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Maracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XFI516

Query Match 7.9%; Score 239; DB 2; Length 1004;

Best Local Similarity 22.0%; Pred. No. 0.00013;  
Matches 158; Conservative 96; Mismatches 293; Indels 172; Gaps 33;

QY 2 NKIYRIIWSNALNAWAVSELTRN-----HTKRASATVATVATLFLFATVQAST 52  
Db 4 NOIYRPNLISLGSVYASHMTNDGCSDVLRHSGVNRNLSVLAIGALTSTVTHAOSVK 63  
QY 53 DDDLLYLEPVGORTA---VLSFRSDKEGTGEKTEVDNS---NWGV----- 91  
Db 64 -----SPAMVTASKVNVAVHVDQVNRUTADRIPTGDGSELMTHMALDWFPPFGNNSIA 116

Qy	92	--YFDKKGVLTAGTIITLKAGDNLKIKQNTN-----ENTNASSFTY-----SLKKDITD	137
Db	117	IGYFSKAFAPNA-----IALGYSVSTQSANNGVALGSGNSTVSGVNSVALGAGMASELNV	172
Qy	138	LTSVGTKEKLSANSKNVITSDTKGLNFAKKTAEFTNGDTPVHLNGIGSTLTDTLTNGCA	197
Db	173	ISVGGGCVTGPVRRIVNV-GDGINNDVAVNKSQLDG-VTASVNDVAASVKTIAL----	226
Qy	198	TTNVTNDNVTDDEKKRAASVKQVLDNLNAGWNIKGVKPGOTTASDNVDFVRYTDTVEFLSADT-	256
Db	227	TNQVTSSSVA-----SASGKESTAIGSGAQAVADNTVAFGGRAITANAVG-ASALGFDSH	279
Qy	257	----KITTNVESKD-----NGKRETVKLGAKTSVIKEKDGKLVTKGD----	295
Db	280	AKGINSTTPTQTSVSLGCGGVSGLGYSNFSVGGESFNGLALGSLVLLQGDVSVALGSGSM	339
Qy	296	-KGENDSSTDKGEG-L-VTAKEVI-----DAVNKAGWRMKTTTANGOTGOADKFEET	343
Db	340	ASEPNVVSVCSGDGLRGPAVRRIVNVGDGINNDVAVNKSQLDGVTASVNDVVASVKNTAG	399
Qy	344	V--TSGTNVTFSAGKGTAT-VSKDQGNITVMYDVNVGDALNVQLQNSGNLND-----	395
Db	400	AIQITSGVASVSGQDSTAAAGSAQAAGDSSIA---LGA SRANAIGSSALGVGDGHALG	455
Qy	396	--SKAVAGSGKVISGVNPSFGKMDETVNIINAGNIEITRNGKNIDITATSMTPQFSVS	453
Db	456	ANSTALGGQSTAISEGGTSLG---YNSFVQGSATNGIALGSN-----AIVSGVNSVA	504
Qy	454	LGAGADAPTLSDDEGALNVGSKD-ANKPV--RITNVAPGVKEGDTVNVQALKGVAQNILN	510
Db	505	LGAGSVASELNV-----ISVGGGCVTGPVARRIVNVGDGINNDVAVNKSQLDGVTASVN	559
Qy	511	N---HIDNVDPGNAR---AGTAAQAI-----ATAGLVQAVLPCKSMMAIG-----	547
Db	560	DVAASVKKIIVGTQITGSGVASAIGKDSATATGASAGAVGSSVALGTRATANAIGSSVLG	619
Qy	548	-----GGTYRGEAGYATGYSSISDGGNWIK-----GTASGNSRGHFGA-SASVGY	592
Db	620	VDSRRAGINSTALGROSNAITGDSGVSIGFNSFVROSGEHGVALGTDAGVSGKDSIALGY	678

RESULT 12

A1477  
190K surface antigen precursor - Rickettsia rickettsii  
C:Species: Rickettsia rickettsii  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 08-Oct-1999  
C:Accession: A1477  
R:Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.  
Infect. Immun. 58, 2760-2769, 1990  
A:Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, ne  
A:Reference number: A1477; MUID:90354033  
A:Accession: A1477  
A:Molecule type: DNA  
A:Residues: 1-2249 <AND>  
A:Cross-references: GB:A13227; NID:g152465; PIDN:AAA26380.1; PID:g152466  
A:Note: the authors translated the codon GAT for residue 430 as Gly, and CAA for residue  
C:Keywords: surface antigen; tandem repeat  
F:1-20/Domain: signal sequence (uncleaved) #status predicted <SIGU>

Query Match 7.4%; Score 224; DB 2; Length 2249;  
Best Local Similarity 24.2%; Pred. No. 0.0021;  
Matches 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34;

[illegible][illegible]

RESULT 13

H83135  
probable adhesin PA4082 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83135  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
;; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: H83135  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1018 <STO>  
A:Cross-references: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AA07469.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4082

Query Match	7.4%	Score 222;	DB 2;	Length 1018;
Best Local Similarity	22.5%;	Pred. No. 0.00097;		
Matches 148;	Conservative	82;	Mismatches 233;	
			Indels 196;	
			Gaps 28;	

Qy	1	MNKYRIIWNALNANWVAVSELTRNHPTKRASATVATAVLATLLFATVQASTTDDDLLEYE	60
Db	1	MKCYALVNWVSQCWNWVSEGSRRGPKAGAKAAATSVLALLGATALAPA-----YAL	54
Qy	61	PVQRATVVLSPRDKECTGSKVEITDSNWGVYEDKKGLVTAGTTILKAGDNLKIKNTNE	120
Db	55	PSGGTV-----GGSGANGRIHLSSGNLSVSNVKDK	85

QY 121 -NTNASSFTYSLAKDLTLDSVTEKLSF---SANSNKVNITSDTKLNFPAKKTAEITNGD 176  
Db 86 LIANWDSFSA-----AGERVIFNPQSSSIALNRVIGTKRASDIQGR-IDANQ 133  
QY 177 T-VHLNGIGSTLTDLLNTGATNV-----TNDNVTDDE-----KKRAASVKVDLN 222  
Db 134 VFLVNPNGV-----LFCRGAQVNVGVLVASTLDTDAEENGSSRYRFTGPGTNGVLN 186  
QY 223 AGNWKGVKPKCTTA-----SDNVFVRYDIVEFLSADTKTTTVNVESKDKNGKREVKIG 277  
Db 187 HGGAITAARGGSIALGAQVDNRCTVLAQMGVGLGAGSDLT-----NFGKNKLLDIRVD 242  
QY 278 AKTSVIEKEKGLVTKGDKGENDSDTKGEGLV---TAKEVIDAVNKAQWRKMTTANGQ 334  
Db 243 AGVANALASNGGL-----KADGGRVLMARATANALLNTVNVNOCALAEASLRK 292  
QY 335 TQO-----ADKFTVTSNTVTFASGKGTATATVSKDDQGNITVMVDVNVGDALNVNQLQ 388  
Db 293 NGRIVLGGPDGKVMYGGALSANALNGFGHGTVEVRQA-----VEVALGTQVNTLA 345  
QY 389 NSGWN-----LDSKAVAGSSGKVI-----SGNVS--PSKG--KMDETVAIN 425  
Db 346 SGNLNGTWKIAADKIDVRSVSDGVTYHADTLSRNLASTNIELVSTKGDLDLDGSVNKA 405  
QY 426 AGNNI-----EITRNGKNIDIATSWTPQFSSVSLGAGADAPTLSDVDDGALNVGSK--- 476  
Db 406 SGNRLGLGSAADLTNGR-----LNASGAKAGLELKABGAIDINDKIVL 449  
QY 477 -----DANKPVRI-----TNVAPGVKEGDVTNVLAQLKGVAQNLNNHID 514  
Db 450 GGAGSALADAGEGHRVNGTASVSLAGANATVYSGGYYTIVVQNLQAQAINKLDG-LY 508  
QY 515 NVDCNARAGTAQAIATAGLVQAYLPCKSMMAIGG--GTYRGE---AGYAIGYSSISDGG 568  
Db 509 VLGCNLLGSGYYCTA-----LQSIGGPAQVFSGLDGLGNSIGNLSISNTG 554  
RESULT 14  
A43855  
high-molecular-weight surface-exposed protein HW1 - Haemophilus influenzae  
C:Species: Haemophilus influenzae  
C>Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: A43855  
R:Barenkamp, S.J.; Leininger, E.  
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus influenzae serotype 100 proteins.  
A:Reference number: A43855; MUID:92192797  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1536 <BAR>  
A:Cross-references: GB:U08876; GB:M84616; PIDN:AAA20527.1; PID:g475771  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)  
Query Match 7.3%; Score 220; DB 2; Length 1536;  
Best Local Similarity 22.7%; Pred. No. 0.0021;  
Matches 130; Conservative 88; Mismatches 210; Indels 144; Gaps 30;  
QY 98 VLTAGTITLAKGDNKLIKONTNENTNASSFTYSLKKDLT-----DLTSY---GTEKLSF 148  
Db 766 VINSKYFNVTGSSLRFTSGSKTKG-----FSIEKDLTLNATGGNITLQVEGIDGMIG 820  
QY 149 SANSNKVNITSDTKLNFPAKTA--ETNGDITVHLNG-----IGSTL-----TDTL 192  
Db 821 KGIYAKNITFEQGNITFGSRKAVTEIEGNTVINNANVTLIGSDFDNHOKPLTIKKDVI 880  
QY 193 LNTGATT---NVTN--DNYTDDKKRAASVKDLNAGWNITKV-----KPGTT 235  
Db 881 INSNLTFAGGNIVNIAGNLTVESN---ANFKAITFTFNVGGFLFDNKGNSNISIAKGGAR 937

QY 236 ASD-----NVDFVRYDIVEFLSADTKTTTVNVESKDKNGKRTVEVKIGAKTSVIEK 286  
Db 938 FKIDNSKNLSITSSSTVRIISGNITNKNGLNITNE--GSDTEMOIGGDSV---QK 992  
QY 287 DGKLVTKDK-----GENSSDTDKGGLVTAK-----EVIDAVNKAQWRKMT 328  
Db 993 EGNLTSSDKNITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNLSGFNKAE 1052  
QY 329 TTAN-----GOTGQADKFEFTVSGTN---VTFASGKGTATATVSKDDQGNITVMVDNV 378  
Db 1053 ITADGSDLTIGNTSAD-----GTNAKVFENQVKDSKISA---DGHKVTLHLSKVET 1102  
QY 379 GDALNVNQ---LNSGWNLDSKAVAGSSGKVISGNSVSPSKGMDETVAINAGNIEITRN 435  
Db 1103 SGSNNNTEDSDNNAGLTIDAKNV-----TVNNNITSHK-----AVSISATSEITTKT 1151  
QY 436 GKNIDIAT---SMTPOFSSVSLGAGADAPTLSDV--DEGALNVGSKDANKPVRITNYPGV 491  
Db 1152 GTTINATTNVETATQGTGILGIESSGSVTLTATEGALAVSNISGN-----TVTFTA 1205  
QY 492 KEGDVTNVA--OLKGY-AQNLNNHIDNVGNARAGIAQAIATAGLVQAYLPCKSMMAIGG 548  
Db 1206 NSGALTTLAGSTIKGTESVTTSSQGDIGGTISGGTVEVRKATESLTT-----QSNKIRA 1260  
QY 549 GTYRGEAGYAIGYSSISDGGNWIIRKTAGSNGS 580  
Db 1261 TT--GEANVTSATGTIG-----GTISGNT 1282  
RESULT 15  
S28634  
adhesin AIDA-I precursor - Escherichia coli plasmid pIB6  
C:Species: Escherichia coli  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 08-Oct-1999  
C:Accession: S28634; S22680; S28881; S72657  
R:Beit, I.  
A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli serotype 104:H21.  
A:Reference number: S22680; MUID:92326638  
A:Accession: S22680  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 839-1286 <BE2>  
A:Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; PID:g42255  
R:Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 6, 1539-1546, 1992  
A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli serotype 104:H21.  
A:Reference number: S22680; MUID:92326638  
A:Accession: S22680  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 839-1286 <BE2>  
A:Cross-references: EMBL:X65022  
A:Experimental source: strain 2787  
A:Accession: S28881  
A:Molecule type: protein  
A:Residues: 50-56 <BE3>  
A:Experimental source: strain 2787  
R:Suhr, M.; Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 22, 31-42, 1996  
A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the out of frame deletion in the AIDA-I precursor.  
A:Reference number: S72657; MUID:97055419  
A:Accession: S72657  
A:Molecule type: protein  
A:Residues: 847-856 <SUH>  
A:Experimental source: DAEC strain 2787  
C:Genetics:  
C:Keywords: membrane protein  
F:1-49/Domain: signal sequence #status predicted <SIG>  
F:50-1286/Product: adhesin AIDA-I #status predicted <MAT>  
Query Match 7.3%; Score 219; DB 2; Length 1286;

```
Best Local Similarity 20.9%; Pred. No. 0.0018;
Matches 146; Conservative 96; Mismatches 256; Indels 202; Gaps 30;

QY 1 MNKIYRIIWNALNAVAVSELRNH-----TKRASATVATA--VLATLLPATVQAST 51
   ||| | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 1 MNKAYSIIWSHRQAVASELARGHGFVLAKNTLLVLAVVSTIGNAFVNIISGTVSSGG 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 52 TDDDLILEPVORTAVYLSFRSDKEGTEVEDSNMGVYFDKKGVLTAGTITLKAGDN 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TVSSG-----ETQIVYS-----GRGNSNATVNSGGTQIVNNGGKTTATVNSSGQN 107
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 112 L-----KIKONTNENTNASSFTYSLK-----132
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 108 VETSGATISTIVNSGGIORVSSGGVASATNLSGGAQNI-YNLGHASNTVIFSGNQTIFS 166
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 133 ---KDLTDLTSVGTCKLSFSAANSKNVITSDTKGLNFAKKTAEKTGDTTVHLN-----182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 GGITDSTNISSGGQQRVSSGGVASNTTINS-----SGAQNILSEGAISTHISGGNQYI 221
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 183 GIGSTLDTLLNTGATNTVNDVTDDKKRAASVKDVLNAGWNKIKVPRPGTTASDNVDF 242
   | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 222 SAGANATEIVNSGGFQRVNSG-----AVATGTVLSGG--TQNVSSGGSAISTSVY 270
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 243 VRTYDVEFLSADTKTTTVNVESKONGKRTVEVIGAKTSVIKEKDKLVTKDKDENDSS 302
   || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 271 NSGVQTV-FAGATVTDTVN--SGGNQNISSGGIVSETTVNVSGTQNIYSG--GSALSA 324
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 303 TDKGGLVTAKEVIDAVNKAQRMKTTTANG-----QTQADKFEFTVSGTNVTFASG-- 355
   || : | : | | | | | | | | | | | | | | | | | | | | | |
Db 325 NIKGSOI-----VNSEGTAINFLVSDGGYQHIRNGGIASGTTIVNOSGYVNISSGGY 375
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 356 -----KGTATVSKDDOGNITVMYD---VNVGD-ALNVNQLNSGWNL-----DSK 397
   : | : | | | | | | | | | | | | | | | | | | | | | | | :
Db 376 AESTIINSGTLRVLSGDYARGTILNNSGRENVSGVSYNAMINTGGNQYIYSDGEATA 435
   | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 398 AVAGSSG--KVISGNVSPSKGMDETVINAGN---NIEITRNGKNI-----DIA 442
   | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 436 AIVNTSGFORINSGGTAPVQNSVYVTRTVSSAAKPPDAEVYSGGKOTVYLWRCIWIYSNEL 495
   | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 443 TSMTPQFSSVSLGAGADAPTLSDVDDGALN-----VG 474
   | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 496 TAVWSMFPGTASGA-----NVNLSGRLNAPAGNVVGTILNQEGRQYVYSGATATSTVG 548
   : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 475 SKDANKPVRITNVAPGVKEGDVTNVAQLKGVQNLNNHIDNVDGNARA-----GIAQAIA 529
   : : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 549 NNEGREVV---LSGGITDGTVLNSGGLQAVSSG-----GKASATVINEGGAQFVY 595
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 530 TAGLVQAYLPGKSMMAIGGTYRGEAGYAGIYSSISDGN 569
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 596 DGGQV----TGTNIK--NGGTIRVDSGASALNIALSSGN 629
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: September 5, 2002, 10:24:32  
Job time: 239 sec

**THIS PAGE BLANK (USPTO)**





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:53 ; Search time 19.11 seconds  
(without alignments)  
1203.528 Million cell updates/sec

Title: US-09-700-293-2

Perfect score: 3019

Sequence: 1 MNKYRIIWSALNAWAVS.....TASGNSRGHFASASGVQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	244	8.1	1039	1 AG43_ECOLI	P39180 escherichia
2	224	7.4	2249	1 OMPA_RICRI	P15921 rickettsia
3	219	7.3	1286	1 AIDA_ECOLI	Q03155 escherichia
4	216.5	7.2	1325	1 YDEK_ECOLI	P32051 escherichia
5	204.5	6.8	1577	1 HLVA_PROMI	P16466 proteus mir
6	203	6.7	1608	1 HLVA_SERMA	P15320 serratia ma
7	198	6.6	2003	1 YDBA_ECOLI	P33866 escherichia
8	195	6.5	1654	1 OMPB_RICRI	Q53047 r outer mem
9	195	6.5	1953	1 BIGA_SALTY	P25927 salmonella
10	194.5	6.4	933	1 SLAP_CAME	P35827 campylobact
11	193	6.4	2021	1 OMPA_RICCN	Q52657 rickettsia
12	192.5	6.4	1645	1 OMPB_RICTY	P96989 r outer mem
13	192.5	6.4	1655	1 OMPB_RICCN	Q9kta3 r outer mem
14	190	6.3	2334	1 WAPA_BACSU	Q07833 bacillus su
15	187	6.2	1569	1 YPUA_ECOLI	P52143 escherichia
16	180.5	6.0	918	1 YMBE_CAEEL	P34487 caenorhabdi
17	176	5.8	1228	1 SLAP_BACST	P35825 bacillus st
18	173	5.7	1300	1 L20K_RICRI	P14914 rickettsia
19	172.5	5.7	1567	1 ICEN_XANCT	P18127 xanthomonas
20	172.5	5.7	3591	1 FHAB_BORPE	P12255 bordetella
21	171.5	5.7	1861	1 APO_THETU	P38536 t anlyopull
22	170.5	5.6	917	1 HXA3_HAEIN	P45355 haemophilus
23	170.5	5.6	1656	1 OMPB_RICJA	Q06653 r outer mem
24	169	5.6	1770	1 PMPC_CHLTR	O84419 chlamydia t
25	167	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
26	165.5	5.5	1036	1 HPI2_DEIRA	P13126 deinococcus
27	165	5.5	642	1 FLID_CAME	Q9phw6 campylobact
28	165	5.5	928	1 HXA2_HAEIN	P45354 haemophilus
29	165	5.5	928	1 PM10_CHLPN	Q9rb65 chlamydia p
30	165	5.5	1007	1 Y741_CHLPU	Q9pj16 chlamydia m
31	164.5	5.4	1025	1 SLAP_CAUCR	P35828 caulobacter
32	163.5	5.4	1276	1 PMP6_CHLPN	Q9z899 chlamydia p
33	162.5	5.4	1167	1 CAGA_HELPJP	Q9zlt1 helicobacte

## ALIGNMENTS

RESULT 1

AG43\_ECOLI

ID AG43\_ECOLI

AC P39180; P76360; P75614; P97241; Q46771;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Antigen 43 precursor (AG43) (Fluffing protein).

GN FLU OR B2000.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI\_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97251358; PubMed=9097040;

RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,

RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,

RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,

RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,

RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,

RA Yamamoto Y., Horiuchi T.;

RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 40.1-50.0 min region on the linkage map.";

RL DNA Res. 3:379-392(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=ML 308-225;

RA Henderson I.R., Owen P.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP PRELIMINARY SEQUENCE OF 53-78.

RC STRAIN=ML 308-225;

RX MEDLINE=89291704; PubMed=2661530;

RA Caffrey P., Owen P.;

RT "Purification and N-terminal sequence of the alpha subunit of antigen

43, a unique protein complex associated with the outer membrane of

Escherichia coli.";

RL J. Bacteriol. 171:3634-3640(1989).

RN [5]

RP SEQUENCE OF 53-63.

RC STRAIN=K12 / EMG2;

RX MEDLINE=97443975; PubMed=9298646;

RA Link A.J., Robison K., Church G.M.;

RT "Comparing the predicted and observed properties of proteins encoded



```
CC EMBL; M31227; AAA26380.1; -.
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 338 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE II).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; A9D6646C089DF087 CRC64;

Query Match 7.4%; Score 224; DB 1; Length 2249;
Best Local Similarity 24.2%; Pred. No. 0.0011;
Matches 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34;

QY 13 LNAWAVSELRN--HTKRASATVATVATLLFATVQASTTDDDDL-----YLEPVQRT 65
DB 640 LNLGALSQVTDIGNTNSLATISVAGTATLGAVIKATTITKNVAVSAVKETNPVVT 699
QY 66 AVVLSFRSDEG---TGEKEVETDSNWGVYFDKKGVLT-----AGTITLKAGNLKIKQN 117
DB 700 GAIDSTGNANNGIVFTGNSVTVDIG-----NTNALATVNVGAGTATL---GGAVIKAT 751
QY 118 TNENTNASSFTYSLKDLTSLTSGTEKLSFSANSKNVITSDTKGLNFAKTAETNGDT 177
DB 752 TTKLTNAASVL-----TLTNAVAVLCAIDNTTGGDNVGV-----LNLGALSQVTDG- 799
QY 178 TVHLNGIGSTLDTLLNTGATTNVTNDV---TDDEKKRAASVKDVLNAGNINIKVPGPT 234
DB 800 -----IGNTNSLATISVAGTATLGAVIKATTITKNVAVSAVKETNPVVT 853
QY 235 TASDNDVFTYDTVEFLSADTKTTTVNVESKDKGTEVKIGAKT-----SVIKEKDGK 289
DB 854 TGGDNVGLNLGALSQVTDIGNT-----NSLAT-ISVAGTATLGAVIKATTITK 904
QY 290 L-----VTGKDKGENDSSTDKEGL 309
DB 905 LTNAASVLTLTNANAVLTGAIDNTTGGDNVGLNLGALSQVTC-DIGNTNSLATISVGA 963
QY 310 VTA-----KEVIDAVNKAGWRMTTANGQTQADKFETVTSGTNTVTFASGKGTATV 362
DB 964 GTATLGAVIKATTITKLTDAASAVKETNPVVTGAIDNTGNANNGI-VTFGTGNSVTGTV 1022
QY 363 SKDDOGNITVMYDYNVDALNVNQLNSGNLDSKAVAGSGKVISGNSVFSKGMDET 422
DB 1023 -----GNTNALATVNVGAGL--LQVGGVVKANTINLTDNASAVTFTNPVVTGAIDNTG 1075
QY 423 NINAG-----NNITRNGKNIDIATSMTPQFSSVSLGAG-----ADAPTLSDVDEG 469
DB 1076 NANGIVFTGNSVTGTVGN-----TNALATVNVGAGLLQVGGVVKANTINLTDNA 1128
QY 470 ALNVGSKDANKPVRITNAPCVKBDVTNVAQLKGAQNLNNHIDNVDGNARA-----GIA 525
DB 1129 S-----AVTFTN-PVWVTGAIDNTG-----NANGIVFTGNSVTGTDIGNT 1169
QY 526 QATAT-----AGL-VQAVLPKSMMA-----IGGTVRGAGYAIGY--- 561
DB 1170 NALATVNVGAGITLQA---GGSLAANNIDFCARSTLEFNGLDGG-----GRAIPYFK 1220
```

```
QY 562 SSISDGNWIIK-----GTASGNSRGH-----FGASASVG 591
DB 1221 GATANGNALNVNTKLLTASHLTIGTVAEINIGAGNLFIDASVG 1266

RESULT 3
AIDA_ECOLI STANDARD; PRT; 1286 AA.
ID AIDA_ECOLI
AC Q03155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aida-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Plasmid pIB6.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (O126:H27);
RX MEDLINE=92326638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X65022; CAA46156.1; -.
DR PIR; S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-I.
FT PROPEP ? 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
```

```
Query Match 7.3%; Score 219; DB 1; Length 1286;
Best Local Similarity 20.9%; Pred. No. 0.001;
Matches 146; Conservative 96; Mismatches 256; Indels 202; Gaps 30;

QY 1 MNKYRIIWSALNAWAVSELRNH-----TKRASATVATA--VLATLLFATVQAST 51
DB 1 MNKAYSIIWSHRSQAVASELARGHGVFLAKNTLLVAVVSTIGNAFVAVISGTVSSGG 60
QY 52 TDDDLKYLEPVQRTAVVLSFRSDEKTEKEVETDSNWGVYFDKKGVLTAGTITLKAGDN 111
DB 61 TVSSG-----ETQIVYS-----GRGNSNATVNSGQTQIVNNGGKTATTAVNSGSGQN 107
QY 112 L-----KIKQNTNENTNASFTYSLK----- 132
DB 108 VGTSGATISTIVNSGGTQVRSSGGVAVSATNLSGGAQNI-YNLGHASNTVIFSGNQITFS 166
QY 133 ---KDLTDLTSVGTPEKLSFSANSKNVITSDTKGLNFAKTAETNGDTTVHLN----- 182
DB 167 GGITDSINISGGQVRSSGGVAVSNNTINS-----SGAQNLSEEGALSTHISGGNQYI 221
QY 183 GIGSTLTDLTNTGATTNVTNDVTDDEKKRAASVKDVLNAGNINIKVPGPTTASDNVDF 242
DB 183 GIGSTLTDLTNTGATTNVTNDVTDDEKKRAASVKDVLNAGNINIKVPGPTTASDNVDF 242
```

Db 222 SAGANATETIVNSGGFQRVNSG-----AVATGTVLSGG--TQNVSSGGSALSTSVY 270  
QY 243 VRTYDVTVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSYKIEKDGKLTGKDKGENSS 302  
Db 271 NSGVQTV-FAGATVTDITVN--SGGNQNISSGGIVSETTVNVSQTNIYSG---GSALSA 324  
QY 303 TDREGVLTAKEIVDAVNAKGRWMTKTANG-----OTGQADKFFETVSGTNVTFASG-- 355  
Db 325 NIKGSQI-----VNSEGTATLVSDGGYQHQHNGGIASGTTVNSGVNVSISGGY 375  
QY 356 -----KGTATVSKDDOGNITVMYD---VNVGD-ALNVNQLONGWNL-----DSK 397  
Db 376 AESTIINSGLTLRLVSDGYARGTILNNSGRENVSNGVSYNAMINTGQNVYISDGRATA 435  
QY 398 AVAGSSG--KVLGSGNVSPSKMDETVNIAGN---NIEITRNGKNI-----DIA 442  
Db 436 AIVNTSGFORINSGETAPQNSVVTVTVSSAAKPFDAEIVYSGGRQTVYLWRGIWYSNFL 495  
QY 443 TSMTPQFSVSLGAGADAPTLVSDDEGALN-----VVG 474  
Db 496 TAVMSFPGTASGA-----NVNLSGRLNAFAGNVVGTILNQEGRVYVSGATATSTVG 548  
QY 475 SKDANKPVRITNVAPGVKEGVDVTVNAOLKGVAQNLNHIDNVGNGARA-----GIAQATA 529  
Db 549 NNEGREYV---LSGITDGTVLNSGGLQAVSSG-----GKASATVINEGAGQFVY 595  
QY 530 TAGLVQALPGLKSMMAIGGTGYRGEAGYATGYSSISDGN 569  
Db 596 DGGQV---TGNTNIK--NGGTIRVDSGASALNALSSGN 629  
  
RESULT 4  
ID YDEK\_ECOLI STANDARD; PRT: 1325 AA.  
AC P32051: P76140; P77168;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical lipoprotein ydek precursor (ORF7).  
GN YDEK OR ORF7 OR B1510.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_Taxid=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sampaio G., Seki Y., Sivasubram S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 595-1325 FROM N.A.  
RX MEDLINE=941100243; PubMed=8274505;  
RA Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoozenraad N.J.;  
RT "An Escherichia coli gene showing a potential ancestral relationship  
to the genes for the mitochondrial import site proteins ISP42 and

RT MOM38.";  
RL Biochim. Biophys. Acta 1153:345-347(1993).  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
CC (Potential).  
CC -!- SIMILARITY: TO E-COLI YFAL.  
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  
CC ISP42 AND MOM38.  
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
CC FRAMESHIFT IN POSITION 653.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: AE000248; AAC74583.1;  
CC EMBL: D50793; BAAL5190.1; ALT\_INIT.  
CC EMBL: D50794; BAAL5197.1; ALT\_INIT.  
CC EMBL: X73295; CAA51730.1; ALT\_FRAME.  
CC PIR: S34315; S34315.  
CC EcoGene: EGI1780; ydek.  
CC PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
CC KW Hypothetical protein; Membrane; Lipoprotein; Signal;  
CC Complete proteome.  
CC FT SIGNAL 1 18 POTENTIAL.  
CC FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.  
CC FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
CC FT CONFLICT 884 884 N -> K (IN REF. 3).  
CC FT CONFLICT 1317 1317 M -> S (IN REF. 3).  
CC SQ SEQUENCE 1325 AA; 136514 MW; 26A3A06FAL9AD7D CRC64;  
  
Query Match 7.2%; Score 216.5; DB 1; Length 1325;  
Best Local Similarity 23.1%; Pred. No. 0.0014;  
Matches 150; Conservative 75; Mismatches 260; Indels 165; Gaps 28;  
  
QY 1 MNKRIYIHSALNNAVAVSELTRNHTKRASATVATVATLFLPATVQASTDDDDLLYLE 60  
Db 1 MNRIYIWNCTLVQVQACSELTRAGKTSTVNLKSSGLTKFESRL----- 47  
QY 61 PVQRTAVVLSFRSDKEGTGEKVEDS-----NWGVYFDK--KGVLTAGTITLKAGDNLKI 114  
Db 48 ----TLGVLLALSGSASGASLEVDNDQITNIDTDVAVDLVGVGTGVLNLAGNLSI 103  
QY 115 KONTNENTNASSFTYSLKKDLTDLTSV--GTEKLSFSANSNK-VNI-TSDTKGLNFAK- 169  
Db 104 -----TTITTSVIGANEDSEGTNVLLGGTWRLYDSGNARPLNVQSGTGTNLKQKG 156  
QY 170 -----TAETNGDTTVHLNGIGSTLTDLLNTGA-----TNTVNDVNDTDEKRAAS 216  
Db 157 HVDGGLRLGSGTGGVTVNVEGDSVLJTELFEGSYGTGSLNIT-----DKGVYVSS 210  
QY 217 VKDVLNAGWNKGVKPGTTASDNVDVFTYDTVEFLSADTKTTTVNVS-----KDNGK 270  
Db 211 IVAL-----GYQAGSNGQ-----VVEKGGEWLKNDS 240  
QY 271 RTEVKIGAKTSVLEKDKGLTKDKDGENSDTDKGLVTAKEVIDAYNKGAWRMKTTT 330  
Db 241 SIEFQIG-----NQGGTEATIREG-GLVTAENTTIGGNATG-----ICT 278  
QY 331 ANQGTQADKFFETVSGTNVTFASGKTGTATVSKDDOGNITVMDVNVGDLN--VNOLQ 388  
Db 279 LNVQ--DQDSVITVVRLLNGYFGNG--TVNISNNGLNINKEYSLVQDGGSHGVNVTD 333  
QY 389 NSGNWL-----DSKAVAGSGKVISGNSVSPSKMDETVNIAGN---- 428  
Db 334 KGHNPLGTGEAFRIYICDAGDGLNVSSEGKVDSGIITAG--MKET---GTGNITVK 387  
QY 429 --NIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLVSDDEGALN-----GSKDANKP 481

```
Db 388 DKSIVITNLGTYDGHGEMNISNOGLVWSNGSSLYGFTGVGNVSIITGGMWEVKN 447
QY 482 VRITNPAVGKGVDTVAQLKQVAAQLNNHNDVGNARAGIAQATATAGLVQAYLP-- 539
Db 448 VYTTIGVAGVGNLISDGG--KFVSQNTIFLGDKASGIGTILNMDATSSFTVGINVGNF 505
QY 540 GKSMATGGGTGYRGEAGYAI-----GYSSIDGGNWIIGKTASGNSR 581
Db 506 GSGIVNVNGATLSTNGTGVGFFGGNAGSGKIVNIISTDSLWNLK-TSSTNAQ 554

RESULT 5
HLXA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RP STRAIN=ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30186; AAA25657.1; -.
DR PIR; A35140;
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.8%; Score 204.5; DB 1; Length 1577;
Best Local Similarity 22.6%; Pred. No. 0.0066;
Matches 149; Conservative 76; Mismatches 257; Indels 177; Gaps 30;

QY 22 LTRNHRKASATVATVATLFLFATVQASTTDDDLYLEPQVQRTAVLVFSRDKEGTGEK 81
Db 317 LTKELGKNIT-----LVASSHNQIKASDLMGDDITLQAGADLT-----DGKQLQOK 364
QY 82 EVTDSNW-----GVYFDKKG-----VLTAGITL-----KAGDNLKI 114
Db 365 ETDIDNRWFYSWKVDYTKESQIQIGSQIDAKNNATLTATKGDVTLDAAKINAGNNLAI 424
QY 115 -----KONTNENTNASSFTYSLKK-----DLTDLT----- 139
```

```
Db 425 NANKDIHINGLVEKESRSENGKRNHTSRLESQGSNSHQETETLKASBELTAGKDLGLDAQ 484
QY 140 -SVTEKLSFSAANSKNYNTSDTKCLNFPAKKTAEINGDTTVHLN-----GIGSLTDLTL 193
Db 485 GSITAQGAHLHANENVLVNAKDNINLVQK-----TNNDKTYTDNHHVMVGGGGGQNNKNN 540
QY 194 NTGATTNVTDNDVTDDEKRAASVKDVLNAGNITKG-----VKPGTTASDNVDVFTYDT 248
Db 541 NQQQVSHAT--QLTADGQLLAAADNNVNITGSQVKGNGQAFVK--TTQGDVVVDNALSET 596
QY 249 VEFLSAD-----TKTTVVNVESKNGKRTVEKIGAKTSVIKEKD-----GKLVYTKDKG 297
Db 597 ISKIDERTGTAFTNITKSSHKNETKQTSGLSELISDAQLTVVSGNDVNVIGSLIKSADKL 656
QY 298 ENDSSTD---KGEGLVT-----AKVIDAVNKGAKWRMKTATTANGOTGOADK 340
Db 657 GIHSLGDNVKSAAQOVTKIDDEKSLAITGHAKEVEDQYSAGFHTHTTNKNTSTETEQ 716
QY 341 FETVTSNTVTFASGKGTATVS--KDOGNITVMYDVNVGDALNVNQLNSGNWNLDSKA 398
Db 717 ANSTISGANVDLQANKOVTFAGSDLKTTAGNASITGD--NVAFVSTENKKQTD--NTDTTI 773
QY 399 VAGSGKVISGNVSPSKGMDVETVINAGNIEITRN--GKNIDIATSMTPQSSVSLGAG 457
Db 774 SGGFS---YTGVDKVGSKADFQYD--KQHTQTEVTKNRGSQTEVAGDLTITANKDLLHEG 829
QY 458 A-----DAPTLSDVDE-----GALNVG-----SKDANKPYR-----IT 485
Db 830 ASHVHEGKYQSGENIQHLVNDSETSKTDSLNVGIDGVNLDYSGVTKPKVKKIAEDGVN 889
QY 486 NVAPGVKEDVTNVAQLKGVAAQNLNN--HIDNVDCNARAGI-----AOAIAFA 531
Db 890 TTKFG--NNTDLTKKVTARDAIANLSNLETNPVGVGVEGKGGSQSQSDQNAVST 947

RESULT 6
HLXA_SERMA STANDARD; PRT; 1608 AA.
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN=SN8;
RX MEDLINE=88257037; PubMed=3290200;
RA Poole K., Schiebel E., Braun V.;
RT "Molecular characterization of the hemolysin determinant of Serratia marcescens.";
RL J. Bacteriol. 170:3177-3188(1988).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC -----
```

```

CC EMBL; M22618; AAA50323.1; -.
DR PIR; A28182; A28182.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 30
FT CHAIN 31 1608
FT SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
SQ
Query Match 6.7%; Score 203; DB 1; Length 1608;
Best Local Similarity 22.9%; Pred. No. 0.008;
Matches 156; Conservative 82; Mismatches 259; Indels 184; Gaps 33;
QY 9 W-NSALNANWAVSELRNH--TKRASATVATAVLATLLFATVQAS---TTDDDLLEPV 62
DB 471 WNSDESESLKASELSEGEELTLKAGNNVSTQ-----CAKVAHQRDLTIDADNQIOGV 524
QY 63 QRTAVVLPSPDSKDECTGEKEVTEDSNWGVYFDKGVLTAGITTLKAGDNLIKONTNENT 122
DB 525 QKTANAKAVRDK-----TSMG-----GIGGGDN-KNNSNRRETS 558
QY 123 NASSFTYSLKDLTDLTSVGTSEKLSFANSKNVIT-SDTKGLNFAKTAETNGDTTVHL 181
DB 559 HAS-----ELTSGGLRLN---GOQGVITGSKARQKGGEVTA--THGGLRID- 602
QY 182 NIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNWKVGPVGTASDNVD 241
DB 603 NALSTVTDKIDARTGTAFTNTSSSHKADNSYQSTASEL-----KSDTNLT 648
QY 242 FVRTYDTVEF-----LSADTKTTTVN-----ESKDNG 269
DB 649 LVSHKADADVIGSQVSGGELSVESKGTGNVKAERQCNIDBQKTLTVNGYAKAGDKQ 708
QY 270 KTEVKI-----GAKTSVIEKDGKLVTC--KDKGENSS-----TDKGEGLVTAKEV 315
DB 709 YRAGLRIRHTRESEKTRTENSASSLSGGSVKLKAEDVTFSGSKLVADGDSVSGNV 768
QY 316 --IDAVNKAGWRMTTANG----QTGQADKFEVTSNTVTFASGKTTATVSK----- 364
DB 769 SFLAADKATASNTQTKIGGFYTGIDK---LGSVEAGYENK-TQASKSATSGS 824
QY 365 DDQGNITVMYDVNVDALYNOLNSGWLKAVAGSGKVGISGVSPSKGMDTVNI 424
DB 825 DVKGNLT-----INARDKLTQOGAGHSVGGAYQENAGVDHUAADTASTTTTIDVGVNI 880
QY 425 NAGNNIETRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDEG-----ALNVGSKD 477
DB 881 -----GANVDYSATVRPERAVGKAALDA-TGVINDIGGIGAPNVLGIDGAOG 928
QY 478 ANKPVRTN---VAPGVKEGDV-----TNVAQLKGAQNINNHIDNVGNARA 522
DB 929 GSSEKRSSSQAVVSSVQAGSIDINAKGEVRDQCTQYQASKG-AVNLTDASHREAAANR 987
QY 523 GIAQAIATAGL--VOAYLPCKSMMAIG---GGTYRGEAGYAGYSGISDGGNW----- 570
DB 988 QDEQSRDTRGSAGVRVYTTTGGDLTVDAKGEQGTQRSNASSASQAVTGSIDAANGINVVK 1047
QY 571 ---IHKGTASGNSRGHFGASA 588
DB 1048 KDAIYOGTALNGGRGKTAVNA.1068
YDBA_ECOLI
RESULT 7
ID YDBA_ECOLI STANDARD; PRT; 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydbA.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

```

```

OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT The complete genome sequence of Escherichia coli K-12.;
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kishimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakano S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12.;
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S-TYPHIMURIUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstations -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000237; AAC74483.1; ALT SEQ.
DR EMBL; AE000237; AAC74487.1; ALT SEQ.
DR EMBL; D90778; BAA15009.1; ALT SEQ.
DR EMBL; D90778; BAA18880.1; ALT SEQ.
DR EMBL; D90779; BAA18881.1; ALT SEQ.
DR EMBL; X62680; -: NOT_ANNOTATED_CDS.
DR EcoGene; EG11307; ydbA.
DR Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;
Query Match 6.6%; Score 198; DB 1; Length 2003;
Best Local Similarity 24.7%; Pred. No. 0.018;
Matches 151; Conservative 74; Mismatches 229; Indels 158; Gaps 35;
QY 32 ATVATAVLATLTFATVQASTTDD-----DLYLEPVORTAVVLSFRS 73
DB 73 STGAALITAT--AVVELNDDDDHHNRNNSPLPTPTDSDDTVPVPTPGDDEIIPDDP 130
QY 74 DKEGTGEKTEVDSNMGVYFDK-KGVLT-----GTTKAGDNLIKONTNE 120
DB 131 DDTPTPKPVSNND--VILDKTEKTLTRDSVFTYTNADGTISLSDSNKGRKATINLWQ 188
QY 121 NTNASSFTYSLKDLTDLTSVGTSEKLSFANSKNVITSDTKGLNFAKTAETNGDTTV 179
DB 121 NTNASSFTYSLKDLTDLTSVGTSEKLSFANSKNVITSDTKGLNFAKTAETNGDTTV 179

```

Db 189 IDEANN-TVALE---GVSADGATKWQYNHNGELY-ITGDNATVNNNGKTTVDGKDSTGT 242  
 Qy 180 HLNG-IGSTLDTLLNT---GATNVNTNDVTDDEKRAASVKDVLNAGWIKGVKPGTT 235  
 Db 243 EINGNNGKVIQDGLDVSGGHHGIDITGDSATVD-NKGTMTVTPESMGIDGDK-AIV 300  
 Qy 236 ASDNVDFVRYTDFEFLSADTKTTTVNVVESKNGK---RTEVKIGAKTSVIKEKDGKL-V 291  
 Db 301 NNEGESTITNGTGTQINGDDATANNNGKTTVDGKDSTGTGTEIN-GNNGKVI--QDGDLDV 357  
 Qy 292 TKDKG---ENDSST--DKGECLYTAREVID-----AVNKAGWRMKTITANGQTGA 338  
 Db 358 SGGGHGIDITGDSATVDNKGKMTVTPESIGIQVDGDAQVYNNEG---ESAITNGGTG-- 412  
 Qy 339 DKFETVTSCTNTPASGRGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLSKA 398  
 Db 413 ----TOINGDDAT-ANNNGKTTVDGKDSTGT-----ITNGGTG-----E 439  
 Qy 399 VAGSSGKVI-SGNVSPSKGMDVETVNNAGNIEITRNGKNIDATSMT---POFSSVSL 454  
 Db 440 IAGNNGKVIQDGLDVSGG-----GHGIDITGDSATVDNKGKMTVTPDPE---SI 485  
 Qy 455 GAGADAPTLSDVDEGALNVGSKDANKPVRIITNVAPGYKEGDTNVVAQLKGVQAQLNNH-I 513  
 Db 486 GIQIDGDAQIYNNEGEST-----ITNGGTG-----TOINGNDATANNNGK 525  
 Qy 514 DNVGDNARAGIAQATATAGLVAOVLPGKSMMAIGGTYRGAGVAGYSSISDGGNWI 573  
 Db 526 TVDGDKSTG-TKAGNIGIYV--LDG-SLIVTGG-----AHGVENIGDNGTYNNK 572  
 Qy 574 GTASGNSRGHFG 585  
 Db 573 GDIVVSDRGSG 584

## RESULT 8

OMP\_RICRI ID OMP\_RICRI STANDARD; PRT; 1654 AA.  
 AC Q53047;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)  
 DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsia;  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=92167802; PubMed=1724278;  
 RA Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;  
 RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia  
 rickettsii is encoded by an unusually long open reading frame:  
 RT evidence for protein processing from a large precursor.";  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 RN [2]  
 RP SEQUENCE OF 279-1654 FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=90136087; PubMed=2515418;  
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the  
 RT 120 kDa surface-exposed protein of Rickettsia rickettsii.";  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY.

CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: X16353; CAA34403.1; --  
 DR InterPro: IPR003858; rOmpA\_rOmpB.  
 DR Pfam: PF02708; rOmpA\_rOmpB; 1.  
 KW Antigen; S-layer; Cell wall.  
 FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.  
 FT DOMAIN 1181 1188 POLY-THR.  
 SO SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;  
 Query Match 6.5%; Score 195; DB 1; Length 1654;  
 Best Local Similarity 21.3%; Pred. No. 0.02;  
 Matches 165; Conservative 93; Mismatches 273; Indels 244; Gaps 36;  
 Qy 30 ASATVATAVLATLLFATVQ-----ASTTDDDDLLLEPVQRTAVYLSFRSDKEGTGE 82  
 Db 20 STATIVASFAGSAGAAIQQRNTTNGAATVDGAGFDQTAAPANVGVALNA-----V 71  
 Qy 83 VTESNMGVYFDK-----KGVL--TAGTITLKAGNLKIKQNTNENTNASTFTYSLK--K 133  
 Db 72 ITANANNGINFTPAGSFNGLLNTANNLAVTVSEDTTIGFTITNVVHNAHSNLTNAGK 131  
 Qy 134 DLTDLTLSVTEKLSFANSKNVI-----TSDTKGL-----NFAK 168  
 Db 132 TLT-ITGCGVTNAQAAATKNAQNVVQFNNGAAIDNNDLKGVGRIDFGAPASTLVFNLAN 190  
 Qy 169 KTAETN---GDTTVHLNGIGSTLTDT-----LLNT----- 195  
 Db 191 PTTQKAPLILGDNAVIANGVNCTLVNTNGFIQVSNKSFATVKAINIADQGIIFNTDANN 250  
 Qy 196 -----GATTNVNDNVTD-----BKRAASVKDVLNA--GNIKGVKPGTTASDNDV 241  
 Db 251 ANTLNLQAGGTINFTGDTGRLVLLSKHAAATNFNITGSLGNLKGVEFTVA----- 306  
 Qy 242 FVRTYDTVEFLSADTKTTVN-----VESKDKG----- 270  
 Db 307 -VDGOLTANAGAAANAVICTNNGAGRAAGFVSVVDNGKVATIDQVYAKDMVIOQSANATGO 365  
 Qy 271 ---RTEVKIGAK-TSVIKEKDKLVTKGDKGENDSSTDKGELVTAKEVIDAV----- 319  
 Db 366 VNRHIVDVGDGTTAFKTAASKVTTQD--SNFGNTDFG-NLAAQIKVPNAITUTGNFT 422  
 Qy 320 -----NKAGWRMKTITANG--QTGQADKFETVTSCTNTPFASCKGT-----TAIVS 363  
 Db 423 GDASNPGTAG--VITFDANGTLESASADANVAVTNITATEASGAGVYVQLSGTHAAELR 480  
 Qy 364 KDDQGNITVMYDVNVGDALN--VNQLNSGNWLSKAVAGSSGKVISGNVSPSKGM--- 418  
 Db 481 LGNAGSIFKLAD---GTVINGKVNQALVGGALAGACTITLDGSAITITDIGNAGAAALQ 537  
 Qy 419 -----DETVNINA--GNNIEITRNGKNI-----DIATSMTPQFS 450  
 Db 538 RITLANDAKKTLTGGANIAGGGGTIDLQANGGTIKLTSTQNNIVVDFDLAIA-TDQTG 596  
 Qy 451 SVSLCAGADAPTLSDVDE-----GALNVSCKD---ANKPVRTNVAPGVKEGDV 496  
 Db 597 VVDASSLNTAOTLTITNGIKGTIGANNKTLGQFNIGSSKTVLSNGVNAINELVIG-NDGAV 655  
 Qy 497 -----TNVAQLKGVQAQLNNHIDVNGNARAGIAQATATAGLVAOYLPGK-----S 542  
 Db 656 QPAHDYTLITRTTNAAGOGKIIFNPVNVNGTTLAAGTNLGSATNPDLAEINFGSKGVNVD 715  
 Qy 543 MMAIGGTYRGAGYA-----IGYSSISDGGNWIKGTASGNSRGHFGASA 588

Db 716 VLVNVEGVNL-----YATNITTTDANGVFVFNAGGTVNIVSGTVGGQGNKENTVA 766

RESULT 9  
BIGA\_SALT  
ID BIGA\_SALT STANDARD; PRT; 1953 AA.  
AC P25927; P25928; Q9XCQ3;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Putative surface-exposed virulence protein bigA precursor.  
GN BIGA OR STM3478.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
NCBI\_TaxID=602;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=14028;  
RC ST011Jkovic I., Valentine P., Heffron F.;  
RA "Salmonella typhimurium rls homolog";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LT2 // SGSC1412 / ATCC 700720;  
RX MEDLINE=21534946; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2.";  
RL Nature 413:852-856(2001).  
RN [3]  
RP SEQUENCE OF 1-765 FROM N.A.  
RC STRAIN=LT2;  
RX MEDLINE=911100301; PubMed=1987123;  
RA Wu J.Y., Siegel L.M., Kredich N.M.;  
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:  
RT requirement for a cloned cysG plasmid to overcome limiting siroheme  
RT cofactor.";  
RL J. Bacteriol. 173:325-333(1991).  
RN [4]  
RP CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
RP in positions 414 and 732.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL: AF133696; AAD39458.1; --  
CC EMBL: AF008859; AAL22340.1; --  
CC EMBL: M64606; AAA27042.1; ALT\_FRAME.  
CC EMBL: M64606; AAA27043.1; ALT\_FRAME.  
CC FIR: C39200; C39200.  
CC FIR: D39200; D39200.  
CC StyGene; SG10437; bigA.  
CC Virulence; Repeat; Signal; Complete proteome.  
KW SIGNAL 1 27  
FT CHAIN 28 1953  
FT PUTATIVE SURFACE-EXPOSED VIRULENCE  
FT PROTEIN BIGA.  
FT DOMAIN 101 252  
FT REPEAT 101 103  
FT REPEAT 104 113  
FT REPEAT 114 122  
FT REPEAT 123 133  
FT REPEAT 134 144  
FT REPEAT 145 155  
FT 15 X 11 AA TANDEM REPEATS.  
FT 1 (INCOMPLETE).  
FT 2 (INCOMPLETE).  
FT 3 (INCOMPLETE).  
FT 4.  
FT 5.  
FT 6.

FT REPEAT 156 166 7.  
FT REPEAT 167 177 8.  
FT REPEAT 178 188 9.  
FT REPEAT 189 199 10.  
FT REPEAT 200 210 11.  
FT REPEAT 211 221 12.  
FT REPEAT 222 232 13.  
FT REPEAT 233 243 14.  
FT REPEAT 244 252 15 (INCOMPLETE).  
FT REPEAT 253 263 16 (INCOMPLETE).  
FT REPEAT 264 274 17 (INCOMPLETE).  
FT REPEAT 275 285 18 (INCOMPLETE).  
FT REPEAT 286 296 19 (INCOMPLETE).  
FT REPEAT 297 307 20 (INCOMPLETE).  
FT REPEAT 308 318 21 (INCOMPLETE).  
FT REPEAT 319 329 22 (INCOMPLETE).  
FT REPEAT 330 340 23 (INCOMPLETE).  
FT REPEAT 341 351 24 (INCOMPLETE).  
FT REPEAT 352 362 25 (INCOMPLETE).  
FT REPEAT 363 373 26 (INCOMPLETE).  
FT REPEAT 374 384 27 (INCOMPLETE).  
FT REPEAT 385 395 28 (INCOMPLETE).  
FT REPEAT 396 406 29 (INCOMPLETE).  
FT REPEAT 407 417 30 (INCOMPLETE).  
FT REPEAT 418 428 31 (INCOMPLETE).  
FT REPEAT 429 439 32 (INCOMPLETE).  
FT REPEAT 440 450 33 (INCOMPLETE).  
FT REPEAT 451 461 34 (INCOMPLETE).  
FT REPEAT 462 472 35 (INCOMPLETE).  
FT REPEAT 473 483 36 (INCOMPLETE).  
FT REPEAT 484 494 37 (INCOMPLETE).  
FT REPEAT 495 505 38 (INCOMPLETE).  
FT REPEAT 506 516 39 (INCOMPLETE).  
FT REPEAT 517 527 40 (INCOMPLETE).  
FT REPEAT 528 538 41 (INCOMPLETE).  
FT REPEAT 539 549 42 (INCOMPLETE).  
FT REPEAT 550 560 43 (INCOMPLETE).  
FT REPEAT 561 571 44 (INCOMPLETE).  
FT REPEAT 572 582 45 (INCOMPLETE).  
FT REPEAT 583 593 46 (INCOMPLETE).  
FT REPEAT 594 604 47 (INCOMPLETE).  
FT REPEAT 605 615 48 (INCOMPLETE).  
FT REPEAT 616 626 49 (INCOMPLETE).  
FT REPEAT 627 637 50 (INCOMPLETE).  
FT REPEAT 638 648 51 (INCOMPLETE).  
FT REPEAT 649 659 52 (INCOMPLETE).  
FT REPEAT 660 670 53 (INCOMPLETE).  
FT REPEAT 671 681 54 (INCOMPLETE).  
FT REPEAT 682 691 55 (INCOMPLETE).  
FT REPEAT 692 701 56 (INCOMPLETE).  
FT REPEAT 702 711 57 (INCOMPLETE).  
FT REPEAT 712 721 58 (INCOMPLETE).  
FT REPEAT 722 731 59 (INCOMPLETE).  
FT REPEAT 732 741 60 (INCOMPLETE).  
FT REPEAT 742 751 61 (INCOMPLETE).  
FT REPEAT 752 761 62 (INCOMPLETE).  
FT REPEAT 762 771 63 (INCOMPLETE).  
FT REPEAT 772 781 64 (INCOMPLETE).  
FT REPEAT 782 791 65 (INCOMPLETE).  
FT REPEAT 792 801 66 (INCOMPLETE).  
FT REPEAT 802 811 67 (INCOMPLETE).  
FT REPEAT 812 821 68 (INCOMPLETE).  
FT REPEAT 822 831 69 (INCOMPLETE).  
FT REPEAT 832 841 70 (INCOMPLETE).  
FT REPEAT 842 851 71 (INCOMPLETE).  
FT REPEAT 852 861 72 (INCOMPLETE).  
FT REPEAT 862 871 73 (INCOMPLETE).  
FT REPEAT 872 881 74 (INCOMPLETE).  
FT REPEAT 882 891 75 (INCOMPLETE).  
FT REPEAT 892 901 76 (INCOMPLETE).  
FT REPEAT 902 911 77 (INCOMPLETE).  
FT REPEAT 912 921 78 (INCOMPLETE).  
FT REPEAT 922 931 79 (INCOMPLETE).  
FT REPEAT 932 941 80 (INCOMPLETE).  
FT REPEAT 942 951 81 (INCOMPLETE).  
FT REPEAT 952 961 82 (INCOMPLETE).  
FT REPEAT 962 971 83 (INCOMPLETE).  
FT REPEAT 972 981 84 (INCOMPLETE).  
FT REPEAT 982 991 85 (INCOMPLETE).  
FT REPEAT 992 1001 86 (INCOMPLETE).  
FT REPEAT 1002 1011 87 (INCOMPLETE).  
FT REPEAT 1012 1021 88 (INCOMPLETE).  
FT REPEAT 1022 1031 89 (INCOMPLETE).  
FT REPEAT 1032 1041 90 (INCOMPLETE).  
FT REPEAT 1042 1051 91 (INCOMPLETE).  
FT REPEAT 1052 1061 92 (INCOMPLETE).  
FT REPEAT 1062 1071 93 (INCOMPLETE).  
FT REPEAT 1072 1081 94 (INCOMPLETE).  
FT REPEAT 1082 1091 95 (INCOMPLETE).  
FT REPEAT 1092 1101 96 (INCOMPLETE).  
FT REPEAT 1102 1111 97 (INCOMPLETE).  
FT REPEAT 1112 1121 98 (INCOMPLETE).  
FT REPEAT 1122 1131 99 (INCOMPLETE).  
FT REPEAT 1132 1141 100 (INCOMPLETE).  
FT REPEAT 1142 1151 101 (INCOMPLETE).  
FT REPEAT 1152 1161 102 (INCOMPLETE).  
FT REPEAT 1162 1171 103 (INCOMPLETE).  
FT REPEAT 1172 1181 104 (INCOMPLETE).  
FT REPEAT 1182 1191 105 (INCOMPLETE).  
FT REPEAT 1192 1201 106 (INCOMPLETE).  
FT REPEAT 1202 1211 107 (INCOMPLETE).  
FT REPEAT 1212 1221 108 (INCOMPLETE).  
FT REPEAT 1222 1231 109 (INCOMPLETE).  
FT REPEAT 1232 1241 110 (INCOMPLETE).  
FT REPEAT 1242 1251 111 (INCOMPLETE).  
FT REPEAT 1252 1261 112 (INCOMPLETE).  
FT REPEAT 1262 1271 113 (INCOMPLETE).  
FT REPEAT 1272 1281 114 (INCOMPLETE).  
FT REPEAT 1282 1291 115 (INCOMPLETE).  
FT REPEAT 1292 1301 116 (INCOMPLETE).  
FT REPEAT 1302 1311 117 (INCOMPLETE).  
FT REPEAT 1312 1321 118 (INCOMPLETE).  
FT REPEAT 1322 1331 119 (INCOMPLETE).  
FT REPEAT 1332 1341 120 (INCOMPLETE).  
FT REPEAT 1342 1351 121 (INCOMPLETE).  
FT REPEAT 1352 1361 122 (INCOMPLETE).  
FT REPEAT 1362 1371 123 (INCOMPLETE).  
FT REPEAT 1372 1381 124 (INCOMPLETE).  
FT REPEAT 1382 1391 125 (INCOMPLETE).  
FT REPEAT 1392 1401 126 (INCOMPLETE).  
FT REPEAT 1402 1411 127 (INCOMPLETE).  
FT REPEAT 1412 1421 128 (INCOMPLETE).  
FT REPEAT 1422 1431 129 (INCOMPLETE).  
FT REPEAT 1432 1441 130 (INCOMPLETE).  
FT REPEAT 1442 1451 131 (INCOMPLETE).  
FT REPEAT 1452 1461 132 (INCOMPLETE).  
FT REPEAT 1462 1471 133 (INCOMPLETE).  
FT REPEAT 1472 1481 134 (INCOMPLETE).  
FT REPEAT 1482 1491 135 (INCOMPLETE).  
FT REPEAT 1492 1501 136 (INCOMPLETE).  
FT REPEAT 1502 1511 137 (INCOMPLETE).  
FT REPEAT 1512 1521 138 (INCOMPLETE).  
FT REPEAT 1522 1531 139 (INCOMPLETE).  
FT REPEAT 1532 1541 140 (INCOMPLETE).  
FT REPEAT 1542 1551 141 (INCOMPLETE).  
FT REPEAT 1552 1561 142 (INCOMPLETE).  
FT REPEAT 1562 1571 143 (INCOMPLETE).  
FT REPEAT 1572 1581 144 (INCOMPLETE).  
FT REPEAT 1582 1591 145 (INCOMPLETE).  
FT REPEAT 1592 1601 146 (INCOMPLETE).  
FT REPEAT 1602 1611 147 (INCOMPLETE).  
FT REPEAT 1612 1621 148 (INCOMPLETE).  
FT REPEAT 1622 1631 149 (INCOMPLETE).  
FT REPEAT 1632 1641 150 (INCOMPLETE).  
FT REPEAT 1642 1651 151 (INCOMPLETE).  
FT REPEAT 1652 1661 152 (INCOMPLETE).  
FT REPEAT 1662 1671 153 (INCOMPLETE).  
FT REPEAT 1672 1681 154 (INCOMPLETE).  
FT REPEAT 1682 1691 155 (INCOMPLETE).  
FT REPEAT 1692 1701 156 (INCOMPLETE).  
FT REPEAT 1702 1711 157 (INCOMPLETE).  
FT REPEAT 1712 1721 158 (INCOMPLETE).  
FT REPEAT 1722 1731 159 (INCOMPLETE).  
FT REPEAT 1732 1741 160 (INCOMPLETE).  
FT REPEAT 1742 1751 161 (INCOMPLETE).  
FT REPEAT 1752 1761 162 (INCOMPLETE).  
FT REPEAT 1762 1771 163 (INCOMPLETE).  
FT REPEAT 1772 1781 164 (INCOMPLETE).  
FT REPEAT 1782 1791 165 (INCOMPLETE).  
FT REPEAT 1792 1801 166 (INCOMPLETE).  
FT REPEAT 1802 1811 167 (INCOMPLETE).  
FT REPEAT 1812 1821 168 (INCOMPLETE).  
FT REPEAT 1822 1831 169 (INCOMPLETE).  
FT REPEAT 1832 1841 170 (INCOMPLETE).  
FT REPEAT 1842 1851 171 (INCOMPLETE).  
FT REPEAT 1852 1861 172 (INCOMPLETE).  
FT REPEAT 1862 1871 173 (INCOMPLETE).  
FT REPEAT 1872 1881 174 (INCOMPLETE).  
FT REPEAT 1882 1891 175 (INCOMPLETE).  
FT REPEAT 1892 1901 176 (INCOMPLETE).  
FT REPEAT 1902 1911 177 (INCOMPLETE).  
FT REPEAT 1912 1921 178 (INCOMPLETE).  
FT REPEAT 1922 1931 179 (INCOMPLETE).  
FT REPEAT 1932 1941 180 (INCOMPLETE).  
FT REPEAT 1942 1951 181 (INCOMPLETE).  
FT REPEAT 1952 1961 182 (INCOMPLETE).  
FT REPEAT 1962 1971 183 (INCOMPLETE).  
FT REPEAT 1972 1981 184 (INCOMPLETE).  
FT REPEAT 1982 1991 185 (INCOMPLETE).  
FT REPEAT 1992 2001 186 (INCOMPLETE).  
FT REPEAT 2002 2011 187 (INCOMPLETE).  
FT REPEAT 2012 2021 188 (INCOMPLETE).  
FT REPEAT 2022 2031 189 (INCOMPLETE).  
FT REPEAT 2032 2041 190 (INCOMPLETE).  
FT REPEAT 2042 2051 191 (INCOMPLETE).  
FT REPEAT 2052 2061 192 (INCOMPLETE).  
FT REPEAT 2062 2071 193 (INCOMPLETE).  
FT REPEAT 2072 2081 194 (INCOMPLETE).  
FT REPEAT 2082 2091 195 (INCOMPLETE).  
FT REPEAT 2092 2101 196 (INCOMPLETE).  
FT REPEAT 2102 2111 197 (INCOMPLETE).  
FT REPEAT 2112 2121 198 (INCOMPLETE).  
FT REPEAT 2122 2131 199 (INCOMPLETE).  
FT REPEAT 2132 2141 200 (INCOMPLETE).  
FT REPEAT 2142 2151 201 (INCOMPLETE).  
FT REPEAT 2152 2161 202 (INCOMPLETE).  
FT REPEAT 2162 2171 203 (INCOMPLETE).  
FT REPEAT 2172 2181 204 (INCOMPLETE).  
FT REPEAT 2182 2191 205 (INCOMPLETE).  
FT REPEAT 2192 2201 206 (INCOMPLETE).  
FT REPEAT 2202 2211 207 (INCOMPLETE).  
FT REPEAT 2212 2221 208 (INCOMPLETE).  
FT REPEAT 2222 2231 209 (INCOMPLETE).  
FT REPEAT 2232 2241 210 (INCOMPLETE).  
FT REPEAT 2242 2251 211 (INCOMPLETE).  
FT REPEAT 2252 2261 212 (INCOMPLETE).  
FT REPEAT 2262 2271 213 (INCOMPLETE).  
FT REPEAT 2272 2281 214 (INCOMPLETE).  
FT REPEAT 2282 2291 215 (INCOMPLETE).  
FT REPEAT 2292 2301 216 (INCOMPLETE).  
FT REPEAT 2302 2311 217 (INCOMPLETE).  
FT REPEAT 2312 2321 218 (INCOMPLETE).  
FT REPEAT 2322 2331 219 (INCOMPLETE).  
FT REPEAT 2332 2341 220 (INCOMPLETE).  
FT REPEAT 2342 2351 221 (INCOMPLETE).  
FT REPEAT 2352 2361 222 (INCOMPLETE).  
FT REPEAT 2362 2371 223 (INCOMPLETE).  
FT REPEAT 2372 2381 224 (INCOMPLETE).  
FT REPEAT 2382 2391 225 (INCOMPLETE).  
FT REPEAT 2392 2401 226 (INCOMPLETE).  
FT REPEAT 2402 2411 227 (INCOMPLETE).  
FT REPEAT 2412 2421 228 (INCOMPLETE).  
FT REPEAT 2422 2431 229 (INCOMPLETE).  
FT REPEAT 2432 2441 230 (INCOMPLETE).  
FT REPEAT 2442 2451 231 (INCOMPLETE).  
FT REPEAT 2452 2461 232 (INCOMPLETE).  
FT REPEAT 2462 2471 233 (INCOMPLETE).  
FT REPEAT 2472 2481 234 (INCOMPLETE).  
FT REPEAT 2482 2491 235 (INCOMPLETE).  
FT REPEAT 2492 2501 236 (INCOMPLETE).  
FT REPEAT 2502 2511 237 (INCOMPLETE).  
FT REPEAT 2512 2521 238 (INCOMPLETE).  
FT REPEAT 2522 2531 239 (INCOMPLETE).  
FT REPEAT 2532 2541 240 (INCOMPLETE).  
FT REPEAT 2542 2551 241 (INCOMPLETE).  
FT REPEAT 2552 2561 242 (INCOMPLETE).  
FT REPEAT 2562 2571 243 (INCOMPLETE).  
FT REPEAT 2572 2581 244 (INCOMPLETE).  
FT REPEAT 2582 2591 245 (INCOMPLETE).  
FT REPEAT 2592 2601 246 (INCOMPLETE).  
FT REPEAT 2602 2611 247 (INCOMPLETE).  
FT REPEAT 2612 2621 248 (INCOMPLETE).  
FT REPEAT 2622 2631 249 (INCOMPLETE).  
FT REPEAT 2632 2641 250 (INCOMPLETE).  
FT REPEAT 2642 2651 251 (INCOMPLETE).  
FT REPEAT 2652 2661 252 (INCOMPLETE).  
FT REPEAT 2662 2671 253 (INCOMPLETE).  
FT REPEAT 2672 2681 254 (INCOMPLETE).  
FT REPEAT 2682 2691 255 (INCOMPLETE).  
FT REPEAT 2692 2701 256 (INCOMPLETE).  
FT REPEAT 2702 2711 257 (INCOMPLETE).  
FT REPEAT 2712 2721 258 (INCOMPLETE).  
FT REPEAT 2722 2731 259 (INCOMPLETE).  
FT REPEAT 2732 2741 260 (INCOMPLETE).  
FT REPEAT 2742 2751 261 (INCOMPLETE).  
FT REPEAT 2752 2761 262 (INCOMPLETE).  
FT REPEAT 2762 2771 263 (INCOMPLETE).  
FT REPEAT 2772 2781 264 (INCOMPLETE).  
FT REPEAT 2782 2791 265 (INCOMPLETE).  
FT REPEAT 2792 2801 266 (INCOMPLETE).  
FT REPEAT 2802 2811 267 (INCOMPLETE).  
FT REPEAT 2812 2821 268 (INCOMPLETE).  
FT REPEAT 2822 2831 269 (INCOMPLETE).  
FT REPEAT 2832 2841 270 (INCOMPLETE).  
FT REPEAT 2842 2851 271 (INCOMPLETE).  
FT REPEAT 2852 2861 272 (INCOMPLETE).  
FT REPEAT 2862 2871 273 (INCOMPLETE).  
FT REPEAT 2872 2881 274 (INCOMPLETE).  
FT REPEAT 2882 2891 275 (INCOMPLETE).  
FT REPEAT 2892 2901 276 (INCOMPLETE).  
FT REPEAT 2902 2911 277 (INCOMPLETE).  
FT REPEAT 2912 2921 278 (INCOMPLETE).  
FT REPEAT 2922 2931 279 (INCOMPLETE).  
FT REPEAT 2932 2941 280 (INCOMPLETE).  
FT REPEAT 2942 2951 281 (INCOMPLETE).  
FT REPEAT 2952 2961 282 (INCOMPLETE).  
FT REPEAT 2962 2971 283 (INCOMPLETE).  
FT REPEAT 2972 2981 284 (INCOMPLETE).  
FT REPEAT 2982 2991 285 (INCOMPLETE).  
FT REPEAT 2992 3001 286 (INCOMPLETE).  
FT REPEAT 3002 3011 287 (INCOMPLETE).  
FT REPEAT 3012 3021 288 (INCOMPLETE).  
FT REPEAT 3022 3031 289 (INCOMPLETE).  
FT REPEAT 3032 3041 290 (INCOMPLETE).  
FT REPEAT 3042 3051 291 (INCOMPLETE).  
FT REPEAT 3052 3061 292 (INCOMPLETE).  
FT REPEAT 3062 3071 293 (INCOMPLETE).  
FT REPEAT 3072 3081 294 (INCOMPLETE).  
FT REPEAT 3082 3091 295 (INCOMPLETE).  
FT REPEAT 3092 3101 296 (INCOMPLETE).  
FT REPEAT 3102 3111 297 (INCOMPLETE).  
FT REPEAT 3112 3121 298 (INCOMPLETE).  
FT REPEAT 3122 3131 299 (INCOMPLETE).  
FT REPEAT 3132 3141 300 (INCOMPLETE).  
FT REPEAT 3142 3151 301 (INCOMPLETE).  
FT REPEAT 3152 3161 302 (INCOMPLETE).  
FT REPEAT 3162 3171 303 (INCOMPLETE).  
FT REPEAT 3172 3181 304 (INCOMPLETE).  
FT REPEAT 3182 3191 305 (INCOMPLETE).  
FT REPEAT 3192 3201 306 (INCOMPLETE).  
FT REPEAT 3202 3211 307 (INCOMPLETE).  
FT REPEAT 3212 3221 308 (INCOMPLETE).  
FT REPEAT 3222 3231 309 (INCOMPLETE).  
FT REPEAT 3232 3241 310 (INCOMPLETE).  
FT REPEAT 3242 3251 311 (INCOMPLETE).  
FT REPEAT 3252 3261 312 (INCOMPLETE).  
FT REPEAT 3262 3271 313 (INCOMPLETE).  
FT REPEAT 3272 3281 314 (INCOMPLETE).  
FT REPEAT 3282 3291 315 (INCOMPLETE).  
FT REPEAT 3292 3301 316 (INCOMPLETE).  
FT REPEAT 3302 3311 317 (INCOMPLETE).  
FT REPEAT 3312 3321 318 (INCOMPLETE).  
FT REPEAT 3322 3331 319 (INCOMPLETE).  
FT REPEAT 3332 3341 320 (INCOMPLETE).  
FT REPEAT 3342 3351 321 (INCOMPLETE).  
FT REPEAT 3352 3361 322 (INCOMPLETE).  
FT REPEAT 3362 3371 323 (INCOMPLETE).  
FT REPEAT 3372 3381 324 (INCOMPLETE).  
FT REPEAT 3382 3391 325 (INCOMPLETE).  
FT REPEAT 3392 3401 326 (INCOMPLETE).  
FT REPEAT 3402 3411 327 (INCOMPLETE).  
FT REPEAT 3412 3421 328 (INCOMPLETE).  
FT REPEAT 3422 3431 329 (INCOMPLETE).  
FT REPEAT 3432 3441 330 (INCOMPLETE).  
FT REPEAT 3442 3451 331 (INCOMPLETE).  
FT REPEAT 3452 3461 332 (INCOMPLETE).  
FT REPEAT 3462 3471 333 (INCOMPLETE).  
FT REPEAT 3472 3481 334 (INCOMPLETE).  
FT REPEAT 3482 3491 335 (INCOMPLETE).  
FT REPEAT 3492 3501 336 (INCOMPLETE).  
FT REPEAT 3502 3511 337 (INCOMPLETE).  
FT REPEAT 3512 3521 338 (INCOMPLETE).  
FT REPEAT 3522 3531 339 (INCOMPLETE).  
FT REPEAT 3532 3541 340 (INCOMPLETE).  
FT REPEAT 3542 3551 341 (INCOMPLETE).  
FT REPEAT 3552 3561 342 (INCOMPLETE).  
FT REPEAT 3562 3571 343 (INCOMPLETE).  
FT REPEAT 3572 3581 344 (INCOMPLETE).  
FT REPEAT 3582 3591 345 (INCOMPLETE).  
FT REPEAT 3592 3601 346 (INCOMPLETE).  
FT REPEAT 3602 3611 347 (INCOMPLETE).  
FT REPEAT 3612 3621 348 (INCOMPLETE).  
FT REPEAT 3622 3631 349 (INCOMPLETE).  
FT REPEAT 3632 3641 350 (INCOMPLETE).  
FT REPEAT 3642 3651 351 (INCOMPLETE).  
FT REPEAT 3652 3661 352 (INCOMPLETE).  
FT REPEAT 3662 3671 353 (INCOMPLETE).  
FT REPEAT 3672 3681 354 (INCOMPLETE).  
FT REPEAT 3682 3691 355 (INCOMPLETE).  
FT REPEAT 3692 3701 356 (INCOMPLETE).  
FT REPEAT 3702 3711 357 (INCOMPLETE).  
FT REPEAT 3712 3721 358 (INCOMPLETE).  
FT REPEAT 3722 3731 359 (INCOMPLETE).  
FT REPEAT 3732 3741 360 (INCOMPLETE).  
FT REPEAT 3742 3751 361 (INCOMPLETE).  
FT REPEAT 3752 3761 362 (INCOMPLETE).  
FT REPEAT 3762 3771 363 (INCOMPLETE).  
FT REPEAT 3772 3781 364 (INCOMPLETE).  
FT REPEAT 3782 3791 365 (INCOMPLETE).  
FT REPEAT 3792 3801 366 (INCOMPLETE).  
FT REPEAT 3802 3811 367 (INCOMPLETE).  
FT REPEAT 3812 3821 368 (INCOMPLETE).  
FT REPEAT 3822 3831 369 (INCOMPLETE).  
FT REPEAT 3832 3841 370 (INCOMPLETE).  
FT REPEAT 3842 3851 371 (INCOMPLETE).  
FT REPEAT 3852 3861 372 (INCOMPLETE).  
FT REPEAT 3862 3871 373 (INCOMPLETE).  
FT REPEAT 3872 3881 374 (INCOMPLETE).  
FT REPEAT 3882 3891 375 (INCOMPLETE).  
FT REPEAT 3892 3901 376 (INCOMPLETE).  
FT REPEAT 3902 3911 377 (INCOMPLETE).  
FT REPEAT 3912 3921 378 (INCOMPLETE).  
FT REPEAT 3922 3931 379 (INCOMPLETE).  
FT REPEAT 3932 3941 380 (INCOMPLETE).  
FT REPEAT 3942 3951 381 (INCOMPLETE).  
FT REPEAT 3952 3961 382 (INCOMPLETE).  
FT REPEAT 3962 3971 383 (INCOMPLETE).  
FT REPEAT 3972 3981 384 (INCOMPLETE).  
FT REPEAT 3982 3991 385 (INCOMPLETE).  
FT REPEAT 3992 4001 386 (INCOMPLETE).  
FT REPEAT 4002 4011 387 (INCOMPLETE).  
FT REPEAT 4012 4021 388 (INCOMPLETE).  
FT REPEAT 4022 4031 389 (INCOMPLETE).  
FT REPEAT 4032 4041 390 (INCOMPLETE).  
FT REPEAT 4042 4051 391 (INCOMPLETE).  
FT REPEAT 4052 4061 392 (INCOMPLETE).  
FT REPEAT 4062 4071 393 (INCOMPLETE).  
FT REPEAT 4072 4081 394 (INCOMPLETE).  
FT REPEAT 4082 4091 395 (INCOMPLETE).  
FT REPEAT 4092 4101 396 (INCOMPLETE).  
FT REPEAT 4102 4111 397 (INCOMPLETE).  
FT REPEAT 4112 4121 398 (INCOMPLETE).  
FT REPEAT 4122 4131 399 (INCOMPLETE).  
FT REPEAT 4132 4141 400 (INCOMPLETE).  
FT REPEAT 4142 4151 401 (INCOMPLETE).  
FT REPEAT 4152 4161 402 (INCOMPLETE).  
FT REPEAT 4162 4171 403 (INCOMPLETE).  
FT REPEAT 4172 4181 404 (INCOMPLETE).  
FT REPEAT 4182 4191 405 (INCOMPLETE).  
FT REPEAT 4192 4201 406 (INCOMPLETE).  
FT REPEAT 4202 4211 407 (INCOMPLETE).  
FT REPEAT 4212 4221 408 (INCOMPLETE).  
FT REPEAT 4222 4231 409 (INCOMPLETE).  
FT REPEAT 4232 4241 410 (INCOMPLETE).  
FT REPEAT 4242 4251 411 (INCOMPLETE).  
FT REPEAT 4252 4261 412 (INCOMPLETE).  
FT REPEAT 4262 4271 413 (INCOMPLETE).  
FT REPEAT 4272 4281 414 (INCOMPLETE).  
FT REPEAT 4282 4291 415 (INCOMPLETE).  
FT REPEAT 4292 4301 416 (INCOMPLETE).  
FT REPEAT 4302 4311 417 (INCOMPLETE).  
FT REPEAT 4312 4321 418 (INCOMPLETE).  
FT REPEAT 4322 4331 419 (INCOMPLETE).  
FT REPEAT 4332 4341 420 (INCOMPLETE).  
FT REPEAT 4342 4351 421 (INCOMPLETE).  
FT REPEAT 4352 4361 422 (INCOMPLETE).  
FT REPEAT 4362 4371 423 (INCOMPLETE).  
FT REPEAT 4372 4381 424 (INCOMPLETE).  
FT REPEAT 4382 4391 425 (INCOMPLETE).  
FT REPEAT 4392 4401 426 (INCOMPLETE).  
FT REPEAT 4402 4411 427 (INCOMPLETE).  
FT REPEAT 4412 4421 428 (INCOMPLETE).  
FT REPEAT 4422 4431 429 (INCOMPLETE).  
FT REPEAT 4432 4441 430 (INCOMPLETE).  
FT REPEAT 4442 4451 431 (INCOMPLETE).  
FT REPEAT 4452 4461 432 (INCOMPLETE).  
FT REPEAT 4462 4471 433 (INCOMPLETE).  
FT REPEAT 4472 4481 434 (INCOMPLETE).  
FT REPEAT 4482 4491 435 (INCOMPLETE).  
FT REPEAT 4492 4501 436 (INCOMPLETE).  
FT REPEAT 4502 4511 437 (INCOMPLETE).  
FT REPEAT 4512 4521 438 (INCOMPLETE).  
FT REPEAT 4522 4531 439 (INCOMPLETE).  
FT REPEAT 4532 4541 440 (INCOMPLETE).  
FT REPEAT 4542 4551 441 (INCOMPLETE).  
FT REPEAT 4552 4561 442 (INCOMPLETE).  
FT REPEAT 4562 4571 443 (INCOMPLETE).  
FT REPEAT 4572 4581 444 (INCOMPLETE).  
FT REPEAT 4582 4591 445 (INCOMPLETE).  
FT REPEAT 4592 4601 446 (INCOMPLETE).  
FT REPEAT 4602 4611 447 (INCOMPLETE).  
FT REPEAT 4612 4621 448 (INCOMPLETE).  
FT REPEAT 4622 4631 449 (INCOMPLETE).  
FT REPEAT 4632 4641 450 (INCOMPLETE).  
FT REPEAT 4642 4651 451 (INCOMPLETE).  
FT REPEAT 4652 4661 452 (INCOMPLETE).  
FT REPEAT 4662 4671 453 (INCOMPLETE).  
FT REPEAT 4672 4681 454 (INCOMPLETE).  
FT REPEAT 4682 4691 455 (INCOMPLETE).  
FT REPEAT 4692 4701 456 (INCOMPLETE).  
FT REPEAT 4702 4711 457 (INCOMPLETE).  
FT REPEAT 4712 4721 458 (INCOMPLETE).  
FT REPEAT 4722 4731 459 (INCOMPLETE).  
FT REPEAT 4732 4741 460 (INCOMPLETE).  
FT REPEAT 4742 4751 461 (INCOMPLETE).  
FT REPEAT 4752 4761 462 (INCOMPLETE).  
FT REPEAT 4762 4771 463 (INCOMPLETE).  
FT REPEAT 4772 4781 464 (INCOMPLETE).  
FT REPEAT 4782 4791 465 (INCOMPLETE).  
FT REPEAT 4792 4801 466 (INCOMPLETE).  
FT REPEAT 4802 4811 467 (INCOMPLETE).  
FT REPEAT 4812 4821 468 (INCOMPLETE).  
FT REPEAT 4822 4831 469 (INCOMPLETE).  
FT REPEAT 4832 4841 470 (INCOMPLETE).



DE S-layer protein (Surface array protein) (SAP).  
GN SAPA.  
OS Campylobacter fetus.  
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
OC Campylobacter.  
OX NCBI\_TaxID=196;  
[1]  
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
RP STRAIN=84-32 / 23D;  
RC MEDLINE=90354448; PubMed=2387868;  
RA Blaser M.J., Gotschlich E.C.;  
RT "Surface array protein of Campylobacter fetus. Cloning and gene  
structure."; J. Biol. Chem. 265:14529-14535(1990).  
RL J. Biol. Chem. 265:14529-14535(1990).  
RN [2]  
RP ERRATUM.  
RX MEDLINE=91035477; PubMed=2229082;  
RA Blaser M.J., Gotschlich E.C.;  
RL J. Biol. Chem. 265:19372-19372(1990).  
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
CC CRITICAL FOR VIRULENCE.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: J05577; AAA23032.1; -  
KW Cell wall; S-layer. F88C729B4BA5B1E9 CRC64;  
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;  
  
Query Match 6.4%; Score 194.5; DB 1; Length 933;  
Best Local Similarity 23.0%; Pred. No. 0.011;  
Matches 151; Conservative 87; Mismatches 238; Indels 181; Gaps 29;  
  
Qy 1 MKYIRIWNAGLNWVAVSELTRNHKRSATVAT-----AVLATL 42  
Db 246 LNAIFATITRAALLTQAEILITRRITNVENIISOLETSGDFVNGYKGFNVLDGI 305  
Qy 43 L-FATVOASTDDDDLYLEPQVRVAVLSFRSDKEGTEKVEDTSNNGVYFDKKGVLTA 101  
Db 306 VSFATDASKVN-----VETGTITAFTA--AGTGKVDV-----AGKLSA 344  
Qy 102 GTITLKAGDNLKIKONTNENTNASFT-YSLK-----KDLTDLTSVGTSEKLSFSANSNKV- 155  
Db 345 LTADSRVSNTLATNDITLTLSANAATSVNLKQKQKDAT-ITSAMQK--YNNRRNR 401  
Qy 156 NITSDTKGLNPAKTAETNGTTHLNL-GIGSTLTDTL-----LNTGATNTVND 204  
Db 402 TITSATAVENLTAKHA-----TNVALNGGMDKLTATVTLDNAALTAADIKSASTLNLS 456  
Qy 205 NVTDE-----KKRAASVKDVLNAGNWKGVKPGTTASDNVDFYR---TYDTV 249  
Db 457 SVNGPKHLYSKRYCKFKRAAAVK--LNT-----TAATDQPTVLKANATNSL 504  
Qy 250 EFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIKEKGLVLTGKDKGENDSSDKGBGL 309  
Db 505 EFDSATKTTVTASG-----SGKTLVKGAEVEVLNID----- 539  
Qy 310 VTAKEVIDAVNAGWRMKTTFANGQTQADKFEFTVTSCTNVTFSAGKGTATVSK--DDQ 367  
Db 540 TTAENALQSV-----SFQKTGGGKF-SVKTGTDKDFEFTVTTTEGSVIDAP 587  
Qy 368 GNITVMDVNVGDALNVNLQNSGNLDSKAVAG---SSGKVISGNVSPSKGMDVTVNI 424  
Db 588 GNDTIAMKSAALTSAFTMIKNIENVAISDAVATADLSAFAKNSVITTTKEAADTTITI 647

Qy 425 NAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRI 484  
Db 648 NKDOVI-----NFTAADAGSVKLITVKLN--DVTALMIVVKIVLDAAKD----- 690  
Qy 485 TNVAPGVKEGDTVTVNAQLKGVAQNLNHNIDVNDGNARAGIAQAATAGLVQAYLPKSGMM 544  
Db 691 TNIALGTAADKALV-----IDGTIELTNISLVKATSPETTANVAKLTDVTSI 741  
Qy 545 AIGG-----GTVRG-----EAGVAIGYSSISDGNWIKTKTASGNS 580  
Db 742 IIDGQITLGHAGTAGTDYSKVSMIDASAKLAKGLTFDASAITLGANATIKGSGADS 798  
  
RESULT 11  
OMPA\_RICCN  
ID OMPA\_RICCN STANDARD; PRT: 2021 AA.  
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;  
AC Q52670; Q52674;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
DE antigen) (rOmpA) (rOmp A).  
GN OMPA OR RC1273.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=941171067; PubMed=8125327;  
RA Crocquet-Valdes P.A., Weiss K., Walker D.H.;  
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia  
RT conorii (Malish 7 strain).";  
RL Gene 140:115-119(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
RL Science 293:2093-2098(2001).  
RN [3]  
RP SEQUENCE OF 8-204 FROM N.A.  
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;  
RX MEDLINE=97015921; PubMed=8662558;  
RA Roux V., Fournier P.E., Raoult D.;  
RT "Differentiation of spotted fever group rickettsiae by sequencing and  
RT analysis of restriction fragment length polymorphism of PCR-amplified  
RT DNA of the gene encoding the protein rOmpA";  
RL J. Clin. Microbiol. 34:2058-2065(1996).  
RN [4]  
RP SEQUENCE OF 953-2012 FROM N.A.  
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;  
RA Raoult D., Fournier P.E., Roux V.;  
RT "Phylogenetic analysis of spotted fever group rickettsiae by study  
RT of the outer surface protein rOmpA";  
RL submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PTM: GLYCOSYLATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial

entitles requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```
CC CC      EMBL; U01028; AAL17405.1; -.
DR DR      EMBL; AEO08674; AAL03811.1; -.
DR DR      EMBL; U43794; AAB49549.1; -.
DR DR      EMBL; U43798; AAB49550.1; -.
DR DR      EMBL; U43806; AAB49551.1; -.
DR DR      EMBL; U45244; AAB49566.1; -.
DR DR      EMBL; U45918; AAB49663.1; -.
DR DR      EMBL; U83440; AAC35176.1; -.
DR DR      EMBL; U83443; AAC35179.1; -.
DR DR      EMBL; U83448; AAC35184.1; -.
DR DR      EMBL; U83453; AAC35189.1; -.
DR DR      InterPro: IP003858; rompA_rompB.
DR DR      Pfam: PF02708; rompA_rompB; 1.
KW KW      Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
KW KW      Complete proteome.
FT FT      SIGNAL          1      38
FT FT      CHAIN           39      2021
FT FT      DOMAIN          238      946
FT FT      DOMAIN          1424     1528
FT FT      VARIANT         60      76
FT FT      VARIANT         76      76
FT FT      VARIANT         86      137
FT FT      VARIANT         126     133
FT FT      VARIANT         953     954
FT FT      VARIANT         1245     1245
FT FT      VARIANT         1308     1308
FT FT      VARIANT         1877     1877
FT FT      CONFLICT        10      10
FT FT      CONFLICT        92      92
FT FT      CONFLICT        126     126
FT FT      CONFLICT        137     137
FT FT      CONFLICT        157     157
FT FT      CONFLICT        368     369
FT FT      CONFLICT        374     388
FT FT      CONFLICT        640     640
FT FT      CONFLICT        669     669
FT FT      CONFLICT        793     793
FT FT      CONFLICT        803     804
FT FT      CONFLICT        809     823
FT FT      CONFLICT        898     898
FT FT      CONFLICT        908     908
FT FT      CONFLICT        985     985
FT FT      CONFLICT       1009    1009
FT FT      CONFLICT       1013    1013
FT FT      CONFLICT       1182    1182
FT FT      CONFLICT       1314    1314
FT FT      CONFLICT       1451    1451
FT FT      CONFLICT       1624    1624
FT FT      CONFLICT       1628    1628
FT FT      CONFLICT       1872    1872
FT FT      CONFLICT       1875    1875
FT FT      CONFLICT       1878    1879
FT FT      CONFLICT       1936    1936
FT FT      CONFLICT       1965    1970
FT FT      CONFLICT       1997    1997
FT FT      SEQUENCE       2021 AA; 203328 MW; 327FC42D7CB24668 CRC64;
Query Match
Best Local Similarity 21.78; DB 1; Length 2021;
Matches 165; Conservative 90; Mismatches 269; Indels 238; Gaps 36;
OY 10 NSALNANWAVSELTRN-HTKRASATVAT-AVLATLLFATVQSTDDDDVLEPQRTAV 67
Db 487 NNGIVFTGDSIVTGNATLATISVGAKATLGAIKATTTKLTID-----NAS 538
OY 68 VLSFRSDKEGTGKEVTEDSNWG-VYDFKKGVLT-----GTITLKG-----DNLKI 114
```

```
Db 539 AVFTNPPVVVTGAIDNTGNANNGIVTFTGDSVTGNTGNATLATISVGAKATLGAI 598
OY 115 KONTNENT-NASSFTYSLRKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKTAFT 173
Db 599 KATTTKLTIDNASAVTFT-----NPVVVTGAIDNTGNANNGIVTFTGNS---IVTGNIGNT 650
OY 174 NGDTTVHLNGIGISTLTDLLNTGATNTVNDNVDDDEKRAASVKDVLNAGNIKGVKPG 233
Db 651 NALATVNV-GAGIATLEGAVIKATTTKLTN-----AASVLTNTVNAVLTGADIN 699
OY 234 TTASDANVDVRYDYVVEFLSADTKTT-----TVNV-----ESKDNG---KRTVEIKGAKTSVI 283
Db 700 TTGVDNVGVNLNGLALSQVTVGNATLATISVGAKATLGAVIKATTTKLTIDNASAV 759
OY 284 KEDGKLVG-----KDKSENSDSTGKGBGLVTAK-----EVIDAVNKA-----GWRMKT 328
Db 760 TFINPPVVVTGAIDNTGNANNGIATFTGDSVTGNTGNATLATVNVVAGLLRVQGVVKS 819
OY 329 TTAN-----GQTQADK-----FETVT---SCTN-----VTFAS 354
Db 820 NTINLTIDNASAVTFTNPVVVTGAIDNTGNANNGIVTFTGDSVTGNTGNATLATISVGA 879
OY 355 GKGT-----TATVSKDDQGNITVMYDVGDLNVNQLNSGNWLDKSAVAGSSGVK 406
Db 880 GKATLGAIKATTTKLTIDNASAVTFTNPVVVTGAID-----NTG-NANNGIVTFTGDS 933
OY 407 ISGNVSPKGMDETVNINAGNIEI--TRNGKNIDIATSMTPQSFSSVSLGAGADAP--- 461
Db 934 VTGNIGNTNAL--ATVNVVAGVTLQAGGSLDANNIDFGARSTLEPNGLDGGNAIPYF 991
OY 462 --TLSVDDEGALNVGSK-----DANK-PVRLTN-----486
Db 992 KGAIANGNNAILNVNTKLTAYHLTIGTVAEINIGAGNLFADASAGDVTILNAQDIFR 1051
OY 487 -----VAPGVKEDV-----TNVAQLKGVQANL 509
Db 1052 ALDSALVLSLTGCVGVNNILLADLVAPGVDEGVTVFGVGNLNGISNA---GAARNI 1108
OY 510 NN-----HIDNVGNARAGIAQIAIA-TAGLVOAYLPKGSMM 544
Db 1109 GDVGKNKENTLLIYNAVITIDVNLNLEGIQNLINNAOFTSTAFNAGTIQ----- 1159
OY 545 ATGGTY-----RGEAGYATGYSSISDGGNWIITKATASGNSR 581
Db 1160 -INDATYTIIDANNGLNIPAGNIKFAHADAQILQNLSSGNDR 1200
RESULT 12
OMPBRICTY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (rompB)
DE (romp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
DE OMPB OR SLP.
GN Rickettsia typhi.
OS Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RX MEDLINE=94040787; PubMed=8224886;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1995).
EN [2]
```



CC SIMILARITY).  
 CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
 CC (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.  
 CC  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AF008659; AAL03623.1;  
 CC EMBL: AF123721; AAF34124.1;  
 CC EMBL: AF123726; AAF34129.1;  
 CC EMBL: AF149110; AAD39533.1;  
 CC InterPro: IPR003858; rOmpA\_rOmpB.  
 CC Pfam: PF02708; rOmpA\_rOmpB; 1.  
 CC Antigen: S-layer; Cell wall; Complete proteome.  
 CC CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.  
 CC CHAIN 1 1335 32 KDA BETA PEPTIDE.  
 CC VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 75 75 K -> S (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
 CC CONFLICT 353 354 KD -> GH (IN REF. 3).  
 CC CONFLICT 776 776 F -> S (IN REF. 3).  
 CC CONFLICT 1159 1159 E -> D (IN REF. 3).  
 CC CONFLICT 1177 1177 G -> S (IN REF. 3).  
 CC CONFLICT 1492 1492 H -> R (IN REF. 3).  
 CC SEQUENCE 1655 AA; 168342 MW; E49E193775D5FCE37 CRC64;

Query Match 6.4%; Score 192.5; DB 1; Length 1655;  
 Best Local Similarity 22.4%; Pred. No. 0.027;  
 Matches 149; Conservative 78; Mismatches 283; Indels 155; Gaps 31;  
 QY 10 NSALNARVAVSELTRNHTKRASATVATVATLTLLEATVOASTDDDDLYLEPVQRTAVVL 69  
 DB 211 NGTLN-----VTNGFKVSKSFATVNVINIGDGMFNTDADNVNTLNLAQANGATI 263  
 QY 70 SFRSDKEGTGEKTEVSDSNWGYFDKKGVLTAGTITLKAGDNLK--IKONT----- 118  
 DB 264 TF-NGTDGTGR-----VLLSKNAARTDFNVTSGLGNLGLIEFNTVAVNGQLKA 313  
 QY 119 NENTNASSFTYSILKDLTDLTSVGTEK-----LSFSANSKV-----NITSDTKGLNF 166  
 DB 314 NAGANAA-----VIGTNNGAGRAAGFVVVDNGKVATIDGVYAKDMVIQS 359  
 QY 167 AKKTAETNGDTVHLNGISLTDLTLNTGATNTVNDVNDVDEKKRAASVKD---VLNA 223  
 DB 360 ANAVGQVNFHIVDGTGTAFATKAVATQNSFGTDFGNLAQIIVPNTMTLNG 419  
 QY 224 GWNKGVKGTTFASDNVDFVRYD---TVFELSADTKTTVN-----VESKNG----- 269  
 DB 420 NFTGDSANFNGTAG-----VTFEDANGTLASASADANVATNTITAIASAGVYVQLSGT 474  
 QY 270 KRETVIGAKTSVIEKDKGLVTKGKENDSDTKGEGLVTAKEVIDAVNKAQGRMKT 329  
 DB 475 HAAELRLGNAGSVFKLADGTVINGK---VNOTALVGGALAAAGTTLDG-----SA 521  
 QY 330 TANGOTGOA-----DKFETVT-----SCTNVTFASGKGTATVSKDDQ 367  
 DB 522 TITGDTIGNAGGAALQGITLANDATKTLTILGGANIICANGGTINFGANGTKIKTS--TQ 579  
 QY 368 GNITVMYDV-----NVGDALNVNQLQNSGWNLDKAVAGSSGKVIKSNVSPSKGKM-D 419

DB 580 NNIVVDFDLAIAFDOTGVVDASSLNAQTLTINGKICTVGANNKTLGOFGNSSKTVLSD 639  
 QY 420 ETVNIN---AGNN--LEITRNGKNIDIAFTMPQ---FSSV-----SLCAGADAPTLVS 465  
 DB 640 GDVAINELVGNNGAVQFAHNYLITRTNAAGOGKIIFNVVNNNTLTATGTLGS-AT 698  
 QY 466 DDEGALNVGSKDANKPVRITNVAPGVKGDVTVNAQLKGVQALNNHNDVVG-NARAGI 524  
 DB 699 NPLAEINFGSKGANVDTVNLNKGKVN--YATNITTTDA---NVGSFIFNAGGTNIIVSG- 753  
 QY 525 AQAIATAGLVQ-----AYLPKSMMAIGGTGVRGAGYAIYGSISDGGNWIIGKGRAS 577  
 DB 754 -----TVGGOGGNKFNVTALDNGTITVKELGNATFNGTNTTAAN-STLQIGGNYTADFVAS 807  
 QY 578 GNSRG 582  
 DB 808 ADGTG 812  
 RESULT 14  
 WAPA\_BACSU  
 ID WAPA\_BACSU STANDARD; PRT; 2334 AA.  
 AC Q07833;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Wall-associated protein precursor.  
 GN WAPA OR N17G.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=168;  
 RX MEDLINE=93302506; PubMed=8316082;  
 RA Foster S.J.;  
 RT "Molecular analysis of three major wall-associated proteins of  
 RT Bacillus subtilis 168: evidence for processing of the product of a  
 RT gene encoding a 258 kDa precursor two-domain ligand-binding  
 RT protein";  
 RL Mol. Microbiol. 8:299-310(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / BGSC1A1;  
 RX MEDLINE=95219088; PubMed=7704263;  
 RA Yoshida K.-I., Sano H., Seki S., Fujimura M., Fujita Y.;  
 RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis  
 RT genome containing the hut and wapa loci";  
 RL Microbiology 141:337-343(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / BGSC1A1;  
 RX MEDLINE=97124196; PubMed=8969509;  
 RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,  
 RA Miwa Y., Fujita Y.;  
 RT "Sequencing of a 65 kb region of the Bacillus subtilis genome  
 RT containing the lic and cel loci, and creation of a 177 kb contig  
 RT covering the gnt-sacxy region";  
 RL Microbiology 142:3113-3123(1996).  
 CC -!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,  
 CC MOTILITY, SECRETION OR DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED  
 CC INTO THE MEDIUM.  
 CC -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE  
 CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE  
 CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED  
 CC MOTIF REPEATED 31 TIMES.  
 CC -!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME  
 CC SIMILARITY TO THE REPEAT IN E.COLI RHE GROUP OF PROTEINS (RHS-A-D).  
 CC  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; L05634; AAA22883.1; -  
DR EMBL; D31856; BAA06656.1; -  
DR EMBL; D29885; BAA06260.1; -  
DR EMBL; D83026; BAA11683.1; -  
DR EMBL; D99124; CAB15959.1; -  
DR PIR; S32920; S32920.  
DR Subtilisin; BG10797; wapa.  
DR InterPro; IPR003305; CBD\_6.  
DR Pfam; PF02018; CBD\_6; 1.  
KW Cell wall; Repeat; Signal; Complete proteome.  
FT SIGNAL 1 28  
FT CHAIN 29 2334  
FT DOMAIN 504 869  
FT REPEAT 504 605  
FT REPEAT 636 736  
FT REPEAT 769 869  
FT DOMAIN 1021 2139  
FT REPEAT 1021 1040  
FT REPEAT 1042 1061  
FT REPEAT 1063 1082  
FT REPEAT 1083 1102  
FT REPEAT 1109 1128  
FT REPEAT 1129 1148  
FT REPEAT 1150 1169  
FT REPEAT 1174 1193  
FT REPEAT 1199 1218  
FT REPEAT 1219 1238  
FT REPEAT 1646 1665  
FT REPEAT 1667 1686  
FT REPEAT 1690 1709  
FT REPEAT 1711 1730  
FT REPEAT 1732 1751  
FT REPEAT 1753 1772  
FT REPEAT 1795 1814  
FT REPEAT 1820 1839  
FT REPEAT 1840 1859  
FT REPEAT 1861 1880  
FT REPEAT 1887 1906  
FT REPEAT 1908 1927  
FT REPEAT 1929 1948  
FT REPEAT 1969 1982  
FT REPEAT 1983 2002  
FT REPEAT 2008 2027  
FT REPEAT 2028 2047  
FT REPEAT 2051 2070  
FT REPEAT 2071 2090  
FT REPEAT 2093 2112  
FT REPEAT 2120 2139  
SQ SEQUENCE 2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;

Query Match 6.3%; Score 190; DB 1; Length 2334;  
Best Local Similarity 23.6%; Pred. No. 0.054;  
Matches 113; Conservative 65; Mismatches 156; Indels 144; Gaps 24;

QY 45 ATVQASTTDDDLVLPVQRTAVVLSFRSDKGTGEK-----EVTEDSN-----W 89  
DB 950 AETSIVTGGMAYID---EDATTHRTTKADGTYQPPGVLELFTETADFLTKYDQT 1006  
QY 90 GYFDFKGGVLTAGTITPLKAGDNLKIKQNTNENTNASSFTYSLKKDLTSLVSGTEKLSFS 149  
DB 1007 NAYFNKKG-----KLQKVVGDHNAIVTYNDKNQLTAITDASGRKLIT 1052  
QY 150 ANSNKVNITSYDKGLNFAKKAETNGDTTVHLNGIGSTITDILLNTGATVNTNDVTD 209

Db 1053 YDENG-HVTSITGPKN--KKV-----TYSYENDLLKKVTD---DGTVTSYDYDSEGR 1100  
QY 210 EKRAASVADVLNAGNKGKPGTTA-----SDNVDFRVYDVTVEFLSADT 256  
Db 1101 VKQYSA-----NSTEAKPVFTTEYQYSGHRLKAKINAKKETVYSYD-----ADK 1144  
QY 257 KTTTVNVESKDNGKRTEV---KIGAKTSVIKEKDGKLVTKGDKGENDS-----STDKE 307  
Db 1145 KTLIM---TOPNGRKVQYGYNEAGNPQIVDDAEGIKTITNTKYEGNVVYEDVDPDVGT 1201  
QY 308 GLVTAKEVIDAVNKAAGRMTTITANGOTGQADKFEVTS-----CTNVTFASCKGTATV 362  
Db 1202 GKAT-----ESYQYDKDGNVTSVKDAYGTE-TYEYNNKNDVT 1238  
QY 363 SKDDOGNIT-VMYDVNVGDALNVQLNSGWNLDKSAVAGSSGKVTSGNVSPSKG-KMDE 420  
Db 1239 MKDTGNTVDIAYD-----GLDAYSETDQSGKSSAAVYDKYGNQIQS 1281  
QY 421 TVNINAGNIEITRNKKNIDIAITSMTPQFSSVSLGAGADAPTLVS--DDEGALNVGSK 476  
Db 1282 SKDLSASTN--ILKDG-----SFEAQSGWNLTASKDKRRKISVIADKSGVLS-GSK 1329  
RESULT 15  
YPUA\_ECOLI  
ID YPUA\_ECOLI STANDARD; PRT: 1569 AA.  
AC P52143; P76610; P77017; P77019;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical outer membrane protein ypuA.  
GN YPUA OR B2647.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RC STRAIN-K12 / MG1655;  
RX MEDLINE-97426617; PubMed-9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE-97349980; PubMed-9205837;  
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,  
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,  
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,  
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
RA Yamagata S., Horiuchi T.;  
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and  
RT analysis of its sequence features.";  
RL DNA Res. 4:91-113(1997).  
CC -|- SUBCELLULAR LOCATION: Outer membrane (Potential).  
CC -|- SIMILARITY: STRONG, TO BORDETTELLA PERTACTIN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U36840; AAA79815.1; ALT\_SEQ.  
DR EMBL; AB000350; AAC75695.1; -.

DR EMBL: D90889; BAA16514.1; ALT\_INIT.  
DR EMBL: D90890; BAA16518.1; ALT\_INIT.  
DR Ecogene; EG13213; ypJA.  
KW Hypothetical protein; Outer membrane  
SQ SEQUENCE 1569 AA; 162774 MW; 0D

Query Match	6.2%	Score 187;	DB 1;	Length 1569;
Best Local Similarity	20.7%;	Pred. No. 0.047;		
Matches 152;	Conservative 87;	Mismatches 262;	Indels 232;	Gaps 35;
QY	41	TLILFTVQASTDDDDLYLEPVORTAVLISFSDREGT-----GEKEVTDNSMGVYFD	94	
Db	534	TVVAKTSAKNIITDGGK-L-IYOKEAKTDSTBLNNGVLEVDGGEAKHVEQSGGALI-	591	
QY	95	KKGVLTAGTI---TLKAGDMLKTKQNTNNT---NASFT-----	128	
Db	592	--ASTTSGTLTEGTSVGDFAFYIRNSEAKNVLENAGSLAVTGTSGRAVDTIINANGKMDV	649	
QY	129	YSLKKDL--TDLTSGVTEKLSFSAANSKNVITSDTK---GL---NFAKKTAEATNGDIT--	178	
Db	650	YG--KDVGTVLNSAGTQTIYASATSKANIIGGQTVYGLATEANIESGEQIVDGGSTPEK	707	
QY	179	YHLNG-----IGSTITDILLMTG-----	205	
Db	708	THINGGTQTVONYGKAIINTDIYSGLOQIMANGTAREGSIINNGSQVYNEGGSLAENVLMDG	767	
QY	206	VTTD--EKKRAASVKDVLNAGWNIGKVPKPTASDNDVFRYDVTFEFLSADTKTTIV--	261	
Db	768	GTLVDREKSGATGIQ-----SSGALVATTTRATRTVTGTGA-DGVAFSIEOGAANNILL	820	
QY	262	-----NVESKONGKRTVEKIGAKTSYIKKK-----	290	
Db	821	ANGGVLTVESDTSDDKTOVNMGGR-EIVKTKATATGTLTGEOIVEGVANETTINDGGI	879	
QY	291	VTGCKDGENSDSTDKEGLVTAKE---VIDAVNKAGWRMKTITANGQTQADKFEVTSG	347	
Db	880	QTVS-ANGFEAIAKTKINEGGTLVNDNGKATDIVQNSGAALQITANG-----TEISG	930	
QY	348	TNY--TFASGCKTTATVSKDDOGNITVMYDVNVGDAL--NVNOLQNSGNLDSKAVAGSS	403	
Db	931	THOYGFHSISGNLAFNMILLENGGNLLVLGATEARDSTVKGKGMQNLG--QDSATKVNSG	988	
QY	404	GKVISQNSVPKCKMDETFINVAGNIETIRNGKIDIAIS-----MTPO-----	448	
Db	989	QOYTLGRSKDEFQALAREDLQVAGTAIVYAGTLADASVSGATGSLSLMTPRDNVTPVK	1048	
QY	449	-----FSSVSLGAGADA--PTLSVDDEGALNVGSKD-----ANKPVRINTPVAPGVK	492	
Db	1049	LEGAVRIITDSATLILGNGVDTTLADTAAASRGVSNLNSNCSAGTSCNCEYRVNSLL--LN	1106	
QY	493	EGDV-----	519	
Db	1107	DGDVYLSAQTAAPATTTIYNLTINELSGSNFYFLHTNVAARGDQLVNVN--NATCN	1163	
QY	520	ARAGIAQAIATAGVQAYLPKGSMAIAGGGYRGEAGYATG-----YSSISDQ	567	
Db	1164	FKI-----FVQDTGVSPQSDAMTLVKYTG-----GDASFLLTGTFVYVYKSKD	1215	
QY	568	-GNWIIKGTASGN	579	
Db	1216	NSNNHLTNDVKPN	1228	

Search completed: September 5, 2002, 10:31:01  
Job time: 428 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 5, 2002, 10:23:18 ; Search time 55.9 Seconds  
(without alignments)  
1838.265 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKIYRIIWNALNAWVAYS.....TASGNSRGHFGASVGYQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rviri:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3019	100.0	594	2	Q93QY4	Q93QY4 neisseria m
2	2931	97.1	594	2	Q9JPI3	Q9JPI3 neisseria m
3	2927	97.0	594	2	Q9JPS2	Q9JPS2 neisseria m
4	2874	95.2	594	2	Q9JPH7	Q9JPH7 neisseria m
5	2863	94.8	598	2	Q9JPR9	Q9JPR9 neisseria m
6	2861	94.8	598	2	Q9JPT0	Q9JPT0 neisseria m
7	2855	94.6	598	2	Q9JPS0	Q9JPS0 neisseria m
8	2852	94.5	598	2	Q93QY5	Q93QY5 neisseria m
9	2806	92.9	600	2	Q9JPS6	Q9JPS6 neisseria m
10	2790	92.4	590	2	Q9JPS3	Q9JPS3 neisseria m
11	2762.5	91.5	599	2	Q9JPR8	Q9JPR8 neisseria m
12	2758.5	91.4	591	2	Q9JPS7	Q9JPS7 neisseria m
13	2758.5	91.4	591	16	Q9JRI8	Q9JRI8 neisseria m
14	2751	91.1	592	2	Q9AQF0	Q9AQF0 neisseria m
15	2739.5	90.7	591	2	Q93QY3	Q93QY3 neisseria m
16	2736.5	90.6	599	2	Q9JPS8	Q9JPS8 neisseria m

17	2718	90.0	598	2	Q9JPR7	Q9JPR7 neisseria m
18	2678	88.7	592	2	Q9JPS9	Q9JPS9 neisseria m
19	2655.5	88.0	595	2	Q9JPH0	Q9JPH0 neisseria m
20	2636	87.3	592	2	Q93QY2	Q93QY2 neisseria m
21	2606	86.3	600	2	Q9JPS5	Q9JPS5 neisseria m
22	2533	83.9	592	16	Q9JQW4	Q9JQW4 neisseria m
23	2527.5	83.7	589	2	Q9JPI0	Q9JPI0 neisseria m
24	2516.5	83.4	589	2	Q93QY1	Q93QY1 neisseria m
25	2444.5	81.0	526	2	Q9JPS4	Q9JPS4 neisseria m
26	2442.5	80.9	530	2	Q9JPS1	Q9JPS1 neisseria m
27	1328.5	44.0	2353	2	P71401	P71401 haemophilus
28	1030	34.1	1098	2	Q48152	Q48152 haemophilus
29	423	14.0	1299	16	Q9F3X6	Q9F3X6 pasteurella
30	398.5	13.2	2059	16	Q9PD50	Q9PD50 xylella fas
31	384.5	12.7	1190	16	Q9PC04	Q9PC04 xylella fas
32	384.5	12.7	2712	16	Q9F3X5	Q9F3X5 pasteurella
33	375.5	12.4	1107	2	Q9F2D8	Q9F2D8 salmonella
34	263	8.7	1291	16	Q92KQ7	Q92KQ7 rhizobium m
35	257.5	8.5	1953	16	Q98HJ2	Q98HJ2 rhizobium l
36	244	8.1	1039	2	Q916T7	Q916T7 escherichia
37	243	8.0	2276	2	Q93TY6	Q93TY6 staphylococ
38	239	7.9	1004	16	Q9PD63	Q9PD63 xylella fas
39	236	7.8	1039	2	Q916T8	Q916T8 escherichia
40	230	7.6	1040	2	Q9AL50	Q9AL50 shigella fl
41	228.5	7.6	1265	2	Q9FDA0	Q9FDA0 xanthomonas
42	228.5	7.6	1557	2	Q9RNI2	Q9RNI2 haemophilus
43	224.5	7.4	989	2	Q9XD84	Q9XD84 escherichia
44	223	7.4	1213	16	Q98JH8	Q98JH8 rhizobium l
45	222	7.4	1018	16	Q9HWU6	Q9HWU6 pseudomonas

ALIGNMENTS

RESULT 1

ID Q93QY4 PRELIMINARY; PRT; 594 AA.  
AC Q93QY4;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG327;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157605; AAK68866.1; -  
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 100.0%; Score 3019; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.2e-118;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60		
Db	1	MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60		
Qy	61	PVQRTAVVLSFRSDKEGTEVTSNMGVYFDKKGVLVTAGTITLKAGDNLIKQNTNE 120		
Db	61	PVQRTAVVLSFRSDKEGTEVTSNMGVYFDKKGVLVTAGTITLKAGDNLIKQNTNE 120		
Qy	121	NTNASSFTYSLKKDLTSLTSVGTETKLSFANSKNKYNITSDTKGLNFAKKTATNGDTTVH 180		
Db	121	NTNASSFTYSLKKDLTSLTSVGTETKLSFANSKNKYNITSDTKGLNFAKKTATNGDTTVH 180		





```
QY 121 NTNASSFTYSLKKDLTDLTSLVTEKLSFSAANSKNVNIITSDTKGLNFAKKTATETNGDITVH 180
|||||
DB 121 NTNASSFTYSLKKDLTDLTSLVTEKLSFSAANSKNVNIITSDTKGLNFAKKTATETNGDITVH 180
|||||
QY 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
|||||
DB 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
|||||
QY 241 DFVRTYDVEFLSADTKTTTVNVESKDKNGKTEVKIGAKTSVIREKDKGLVTGDKDGEND 300
|||||
DB 241 DFVRTYDVEFLSADTKTTTVNVESKDKNGKTEVKIGAKTSVIREKDKGLVTGDKDGEND 300
|||||
QY 301 SSTDKGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTFFASGKTGA 360
|||||
DB 301 SSTDKGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTFFASGKTGA 360
|||||
QY 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMD 420
|||||
DB 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMD 420
|||||
QY 421 TVNINAGNNIEITRNKKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 480
|||||
DB 421 TVNINAGNNIEITRNKKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 480
|||||
QY 481 PVRITNAPGVKEGDVTNVAQLKGVAQNLNHNIDNVGDNARAGTAQAATATAGLVQAYLPG 540
|||||
DB 481 PVRITNAPGVKEGDVTNVAQLKGVAQNLNHNIDNVGDNARAGTAQAATATAGLVQAYLPG 540
|||||
QY 541 KSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594
|||||
DB 541 KSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594
|||||

RESULT 4
Q9JPH7 PRELIMINARY; PRT; 594 AA.
ID Q9JPH7 AC Q9JPH7
RX STRAIN=B2198, AND 297-0; MEDLINE=20175756; PubMed=10710308;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NIHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198, AND 297-0; MEDLINE=20175756; PubMed=10710308;
RX STRAIN=B2198;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226368; AAF42517.1; -
DR EMBL; AF226358; AAF42507.1; -
DR EMBL; AF157604; AAF68865.1; -
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE682635C CRC64;
```

```
Query Match 95.2%; Score 2874; DB 2; Length 594;
Best Local Similarity 95.6%; Pred. No. 1.3e-112;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKYRIIWNALNAWAVAYSELTRNHTKRASATVATAVLATLLFATVOASTDDDDLLYLE 60
|||||
DB 1 MNKYRIIWNALNAWAVAYSELTRNHTKRASATVATAVLATLLFATVOANATDDDDLLYLE 60
|||||
QY 61 PVQRTAVVLSFRSDEKTEGTEVDSNNGVYFDEKKGVLTAGTITLTKAGDNLKIKQNTNE 120
|||||
DB 61 PVQRTAVVLSFRSDEKTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEG 120
|||||
QY 121 NTNASSFTYSLKKDLTDLTSLVTEKLSFSAANSKNVNIITSDTKGLNFAKKTATETNGDITVH 180
|||||
DB 121 NTNASSFTYSLKKDLTDLTSLVTEKLSFSAANSKNVNIITSDTKGLNFAKKTATETNGDITVH 180
|||||
QY 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
|||||
DB 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
|||||
QY 241 DFVRTYDVEFLSADTKTTTVNVESKDKNGKTEVKIGAKTSVIREKDKGLVTGDKDGEND 300
|||||
DB 241 DFVRTYDVEFLSADTKTTTVNVESKDKNGKTEVKIGAKTSVIREKDKGLVTGDKDGEND 300
|||||
QY 301 SSTDKGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTFFASGKTGA 360
|||||
DB 301 SSTDKGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTFFASGKTGA 360
|||||
QY 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMD 420
|||||
DB 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMD 420
|||||
QY 421 TVNINAGNNIEITRNKKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 480
|||||
DB 421 TVNINAGNNIEITRNKKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 480
|||||
QY 481 PVRITNAPGVKEGDVTNVAQLKGVAQNLNHNIDNVGDNARAGTAQAATATAGLVQAYLPG 540
|||||
DB 481 PVRITNAPGVKEGDVTNVAQLKGVAQNLNHNIDNVGDNARAGTAQAATATAGLVQAYLPG 540
|||||
QY 541 KSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594
|||||
DB 541 KSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594
|||||

RESULT 5
Q9JPR9 PRELIMINARY; PRT; 598 AA.
ID Q9JPR9 AC Q9JPR9
RX STRAIN=NGH36; MEDLINE=20175756; PubMed=10710308;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36; MEDLINE=20175756; PubMed=10710308;
RX STRAIN=NGH36;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
```

DR EMBL; AF226359; AAF42508.1; -. 63A6A3BD7F0F2EE3 CRC64;  
SQ SEQUENCE 598 AA: 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 94.8%; Score 2861; DB 2; Length 598;  
Best Local Similarity 94.8%; Pred. No. 4.6e-112;  
Matches 567; Conservative 5; Mismatches 22; Indels 4; Gaps 1;

Qy 1 MNKIYRIWNSALNAWAVSELTRNTHKRASATVATAVLATLLFAIVQASTTDDDDLYLE 60  
Db 1 MNKIYRIWNSALNAWVVSELTNRHTRKASATVATVATLTLFAIVQANATDDDDLYLE 60  
Qy 61 PVQRTAVLSFRSDKEGTEGEVTEDSNWGVYFDKKGLVTAGTTILKAGDNLKIKONTNE 120  
Db 61 PVQRTAVLSFRSDKEGTEGEVTEDSNWA VYFDEKRVLKAGAITLTKAGDNLKIKONTNE 120  
Qy 121 NTNA-----SSFTYSLLKKDLTDLTSGVTEKLISFSANSKNVNITSDPTKLNFAAKTAETNGD 176  
Db 121 NTNENTNDSSFTYSLLKKDLTDLTSTVETEKLISFGANGKNYNITSDTKLGNFAKETAGTNGD 180  
Qy 177 TTVHLANGICSTLDTPLLNTGATTNNVDNVDTDEKKRAASKDVLNAGWNINVKVPQTGA 236  
Db 181 PTVHLANGICSTLDTPLLNTGATTNNVDNVDTDEKKRAASKDVLNAGWNINVKVPQTGA 240  
Qy 237 SDNVDFVRIDVFELSDADTKTTTNVESDKDNKRPTEVKIGAKTSVIEKDGKLVTKDK 296  
Db 241 SDNVDFVRIDVFELSDADTKTTTNVESDKDNKRPTEVKIGAKTSVIEKDGKLVTKGK 300  
Qy 297 GENSDTSKGRLVTAKEVIDAVNKAAGRWMKTITTANGQTGOADKFETVTSIGNVTFFASGK 356  
Db 301 GENGSTDEBGLVTAKEVIDAVNKAAGRWMKTITTANGQTGOADKFETVTSIGKVTTFASGN 360  
Qy 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLONGSNWLDSKAVAGSSGKVISGNYSPSKG 416  
Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLONGSNWLDSKAVAGSSGKVISGNYSPSKG 420  
Qy 417 KMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLAGAGADAPTLSVDDEGALNVGSK 476  
Db 421 KMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLAGAGADAPTLSVDDEGALNVGSK 480  
Qy 477 DANKPVRIITNPAPGVKGGDVNVLAQLKGVAQNLNHNIDNVGNARAGIAQAATAGLVQA 536  
Db 481 DANKPVRIITNPAPGVKGGDVNVLAQLKGVAQNLNHRIDNVGNARAGIAQAATAGLAQA 540  
Qy 537 YLPKGSMAIAGCGTYRGEGAYGAIYCSISDPGNNIIKGTASGNSRGHFASASVGYYQW 594  
Db 541 YLPKGSMAIAGCGTYRGEGAYGAIYCSISDTPGNNVIKGTASGNSRGHFCTASVGYYQW 598

RESULT 7  
QJPSO PRELIMITINARY; PRG; 598 AA.  
ID QJPSO PRELIMITINARY; PRG; 598 AA.  
DC 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2000 (TREMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxId=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH15;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzo M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Saviano S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tetzelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Mezon E.R., Grandi G., Rappuoli R.;  
RT \*Identification of Vaccine Candidates Against Serogroup B

Query Match	94.8%	Score 2863	DB 2	Length 598
Best local similarity	95.0%	Prod. NO. 3.8e-112		
Matches 566	Conservative	5	Mismatches 21	Indels 4
Gaps				
QY	1	MNKYRIIWSALNAWVSELTRNRHTRKASATVATVAVLATLTLFATVOASTDDDDLYLE	60	
DB	1	MNKYRIIWSALNAWVSELTRNRHTRKASATVATVAVLATLTLFATVOANATDDDDLYLE	60	
QY	61	PVQRTAVVLVSFRSDKEGTEKVEDTSDNWGVYEDKKGYLVLTAGTITLAKAGDNLKIKONTNE	120	
DB	61	PVQRTAVVLVSFRSDKEGTEKVEDTSDNWGVYEDKKGYLVLTAGTITLAKAGDNLKIKONTNE	120	
QY	121	NTNA-----SFTYSLSKKDLDTLSVTGTEKLSFSAANSKNVITSDTKGLNFAKTAETNGD	176	
DB	121	NTNENTNDSFTYSLSKKDLDTLSVETEKLSFGANGKNVITSDTKGLNFAKETAETNGD	180	
QY	177	TVHLNGIGSTLTDLTLLNTGATVNTVNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA	236	
DB	181	PTVHLNGIGSTLTDLTLLNTGATVNTVNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA	240	
QY	237	SDNVDFVRTYDVTVEFLSDADTKTTNVNYESKDNCKRTEYKIGAKTSVKEKDGKLVTKDCK	296	
DB	241	SDNVDFVRTYDVTVEFLSDADTKTTNVNYESKDNCKRTEYKIGAKTSVKEKDGKLVTKGCK	300	
QY	297	GENDSSTDKGEGVLTAKEVIDAVNKAQWRMKTITANGOTQADKFEVTSCTNVTFSASK	356	
DB	301	DENGSSTDEGEGVLTAKEVIDAVNKAQWRMKTITANGOTQADKFEVTSCTNVTFSASK	360	
QY	357	GTTATVTSKDDQGNITVMKDVNVGVALVNLQNSGWNLDKSAVAGSSGKVIISGNVSPSKG	416	
DB	361	GTTATVTSKDDQGNITVMKDVNVGVALVNLQNSGWNLDKSAVAGSSGKVIISGNVSPSKG	420	
QY	417	KMDVTVINAGNNIEITRNGKNIDIASTWTPQPSVSVLGAGADAPTILSVDDGALNVGSK	476	
DB	421	KMDVTVINAGNNIEITRNGKNIDIASTWTPQPSVSVLGAGADAPTILSVDDGALNVGSK	480	
QY	477	DANKPVRITNVAQVKEGSDVTNVLAQLKGVAAQNIINNHNDVGNARAGIAQIAITAGLVQA	536	
DB	481	DTNKPVRITNVAQVKEGSDVTNVLAQLKGVAAQNIINNHNDVGNARAGIAQIAITAGLVQA	540	
QY	537	YLPCKSMMAITGGGTGGEAGYAIYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594	
DB	541	YLPCKSMMAITGGGTGGEAGYAIYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	598	
RESULT	6			
Q9JPT0				
ID	Q9JPT0	PRELIMINARY:	PRT:	598 AA.
DC	Q9JPT0:			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)			
DE	OUTER MEMBRANE PROTEIN GNA992.			
GN	GNA992			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_taxonomy:487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-25962;			
RC	MEDLINE-20175756; PubMed-10710308;			
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,			
RA	Galeotti C.B., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,			
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,			
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,			
RA	Moxon E.R., Grandi G., Rappuoli R.			
RT	*Identification of Vaccine Candidates Against serogroup B			
RT	Meningococcus by Whole-Genome Sequencing.*			
RT	Science 287:1816-1820(2000).			

RT Meningococcus by Whole-Genome Sequencing.";  
RN Science 287:1816-1820(2000).  
RL [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=H15;

RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of *Neisseria meningitidis*.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF226381; AAF42530.1; -  
DR EMBL; AF157607; AAK68868.1; -  
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8BA63CB CRC64;

Query Match 94.6%; Score 2855; DB 2; Length 598;  
Best Local Similarity 94.6%; Pred. No. 8.2e-112;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIWNSALNAWVAVSELTRNHTKRASATVATATLTLFATVQASTTDDDDLYLE 60  
DB 1 MNKISRIWNSALNAWVAVSELTRNHTKRASATVATATLTLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKTEDESNWGVYFDKGVLTAGTITLKAGNLKIKQNTNE 120  
DB 61 PVQRTAVVLSFRSDKEGTGEKTEDESNWGVYFDEKRVLKAGAITLKAGNLKIKQNTNE 120  
QY 121 NTNA----SSFTYSLKKDLTSLTSGTEKLSFSAANSKNVNTSDTKGLNFAKKAETNGD 176  
DB 121 NTNENTNDSFTYSLKKDLTSLTSGTEKLSFGANGKNVNTSDTKGLNFAKKAETNGD 180  
QY 177 TTVHLNGIGSTLTDLTLLTNGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236  
DB 181 PTVHLNGIGSTLTDLTLLTNGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240  
QY 237 SDNVDFVRTYDTEFLSADTKTTTVNVESKDNKRTKTEVKGAKTSVKEKDGKLVTKGDK 296  
DB 241 SDNVDFVRTYDTEFLSADTKTTTVNVESKDNKRTKTEVKGAKTSVKEKDGKLVTKGDK 300  
QY 297 GENDSSDCKEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEFVTSCTNVTTFASGK 356  
DB 301 DENGSSDCKEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEFVTSCTNVTTFASGN 360  
QY 357 GTTATVSKDDQGNITVYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
DB 361 GTTATVSKDDQGNITVYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 417 KMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
DB 421 KMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTNVNVAQLKGVQNLNHHIDNVGNARAGIAQAIATAGLVQA 536  
DB 481 DANKPVRITNVAPGVKEGDTNVNVAQLKGVQNLNHHIDNVGNARAGIAQAIATAGLVQA 540  
QY 537 YLPCKSMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRHFSGASVGYQW 594  
DB 541 YLPCKSMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRHFSGASVGYQW 598

RESULT 8  
Q93QY5 ID Q93QY5 PRELIMINARY; PRT; 598 AA.  
AC Q93QY5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.

OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=BZ10;  
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of *Neisseria meningitidis*.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157603; AAK68864.1; -  
SQ SEQUENCE 598 AA; 62687 MW; 18CEFF6410A15DF CRC64;

Query Match 94.5%; Score 2852; DB 2; Length 598;  
Best Local Similarity 94.6%; Pred. No. 1.1e-111;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIYRIWNSALNAWVAVSELTRNHTKRASATVATATLTLFATVQASTTDDDDLYLE 60  
DB 1 MNKISRIWNSALNAWVAVSELTRNHTKRASATVATATLTLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKTEDESNWGVYFDKGVLTAGTITLKAGNLKIKQNTNE 120  
DB 61 PVQRTAVVLSFRSDKEGTGEKTEDESNWGVYFDEKRVLKAGAITLKAGNLKIKQNTNE 120  
QY 121 NTNA----SSFTYSLKKDLTSLTSGTEKLSFSAANSKNVNTSDTKGLNFAKKAETNGD 176  
DB 121 NTNENTNDSFTYSLKKDLTSLTSGTEKLSFGANGKNVNTSDTKGLNFAKKAETNGD 180  
QY 177 TTVHLNGIGSTLTDLTLLTNGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236  
DB 181 PTVHLNGIGSTLTDLTLLTNGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240  
QY 237 SDNVDFVRTYDTEFLSADTKTTTVNVESKDNKRTKTEVKGAKTSVKEKDGKLVTKGDK 296  
DB 241 SDNVDFVRTYDTEFLSADTKTTTVNVESKDNKRTKTEVKGAKTSVKEKDGKLVTKGDK 300  
QY 297 GENDSSDCKEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEFVTSCTNVTTFASGK 356  
DB 301 GENGSSDCKEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEFVTSCTNVTTFASGN 360  
QY 357 GTTATVSKDDQGNITVYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
DB 361 GTTATVSKDDQGNITVYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 417 KMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
DB 421 KMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTNVNVAQLKGVQNLNHHIDNVGNARAGIAQAIATAGLVQA 536  
DB 481 DANKPVRITNVAPGVKEGDTNVNVAQLKGVQNLNHHIDNVGNARAGIAQAIATAGLVQA 540  
QY 537 YLPCKSMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRHFSGASVGYQW 594  
DB 541 YLPCKSMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRHFSGASVGYQW 598

RESULT 9  
Q9JPS6 ID Q9JPS6 PRELIMINARY; PRT; 600 AA.  
AC Q9JPS6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.

OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masiagnani V., Giulliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.,  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226371; AAF42520.1; -;  
 SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 92.9%; Score 2806; DB 2; Length 600;  
 Best Local Similarity 92.7%; Pred. No. 9.1e-110;  
 Matches 557; Conservative 14; Mismatches 22; Indels 8; Gaps 2;

Qy 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFAT-----VQASTTD 53  
 Db 1 MNKIYRIIWNALNAWVSELTRNHTKRASATVETAVLATLFLFATVQASADNVQASADN 60  
 Qy 54 DDOLYLEPQRTAVVLSFRSDEKGTGEKTEVSDNSNGVYFDKRGVLTAGTITLKGONLKL 113  
 Db 61 EEEYLEPVRTAPVLSFYDAEDTGEKTEVNTNGVYFDKRGVLTAGTITLKGONLKL 120  
 Qy 114 IKONTENTNASSFTYSLKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKTAET 173  
 Db 121 IKONTENTNASSFTYSLKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKTAET 180  
 Qy 174 NGDTTVHLNGIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNKGKVPK 233  
 Db 181 NGDTTVHLNGIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNKGKVPK 240  
 Qy 234 TTASDNVDFRYDYVEFLSADTKTTVNVESKDNKRTVEKIGAKTSVIEKDGKLVG 293  
 Db 241 TTASDNVDFRYDYVEFLSADTKTTVNVESKDNKRTVEKIGAKTSVIEKDGKLVG 300  
 Qy 294 KDKGENDSTDKGEGLVTAKEVIDAVNKGARMKTTTANGQTKQADKFTVTSNTVFA 353  
 Db 301 KKGEGNSTDKGEGLVTAKEVIDAVNKGARMKTTTANGQTKQADKFTVTSNTVFA 360  
 Qy 354 SGKGTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWLDKAVAGSSGKVIISGNVSP 413  
 Db 361 SGKGTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWLDKAVAGSSGKVIISGNVSP 420  
 Qy 414 SKGMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNV 473  
 Db 421 SKGMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALNV 479  
 Qy 474 GSKDANKPVRITNVAPGVKEGDTNVQNLQNSGNWLDKAVAGSSGKVIISGNVSP 533  
 Db 480 GSKDANKPVRITNVAPGVKEGDTNVQNLQNSGNWLDKAVAGSSGKVIISGNVSP 539  
 Qy 534 VQAYLPCKSMAIGGTYRGAGYAGYSSTDSGGNWIKGTASGNSRCHFCASASVGYO 593  
 Db 540 VQAYLPCKSMAIGGTYRGAGYAGYSSTDSGGNWIKGTASGNSRCHFCASASVGYO 599  
 Qy 594 W 594  
 Db 600 W 600

RESULT 10  
 Q9JPS3 ID Q9JPS3 PRELIMINARY; PRT; 590 AA.  
 AC Q9JPS3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=NCE28;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Galeanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Casetti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuki S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.,  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226378; AAF42527.1; -;  
 SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 92.4%; Score 2790; DB 2; Length 590;  
 Best Local Similarity 93.5%; Pred. No. 4.1e-109;  
 Matches 557; Conservative 12; Mismatches 19; Indels 8; Gaps 3;

Qy 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASATDDDDLY-L 59  
 Db 1 MNKIYRIIWNALNAWVSELTRNHTKRASATVETAVLATLFLFATVQASADNVQASADN 60  
 Qy 60 EPQRTAVVLSFRSDEKGTGEKE-VTDSNNGVYFDKRGVLTAGTITLKGONLKI 118  
 Db 61 DPQRTAVVLSFRSDEKGTGEKE-VTDSNNGVYFDKRGVLTAGTITLKGONLKI 118  
 Qy 119 NEWTNASSFTYSLKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKTAETNGDTT 178  
 Db 119 ----NGTNTYSLKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKTAETNGDTT 174  
 Qy 179 VHLNGIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNKGKVPKPTASD 238  
 Db 175 VHLNGIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNKGKVPKPTASD 234  
 Qy 239 NVDFRYDYVEFLSADTKTTVNVESKDNKRTVEKIGAKTSVIEKDGKLVGKGE 298  
 Db 235 NVDFRYDYVEFLSADTKTTVNVESKDNKRTVEKIGAKTSVIEKDGKLVGKGE 294  
 Qy 299 NDSTDKGEGLVTAKEVIDAVNKGARMKTTTANGQTKQADKFTVTSNTVFA 358  
 Db 295 NGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGQTKQADKFTVTSNTVFA 354  
 Qy 359 TATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGM 418  
 Db 355 TATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGM 414  
 Qy 419 DETVNTNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDA 478  
 Db 415 DETVNTNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDA 474  
 Qy 479 NKPVRTNVAPGVKEGDTNVQNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGM 538  
 Db 475 NKPVRTNVAPGVKEGDTNVQNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGM 534  
 Qy 539 PGKSMMAIGGTYRGAGYAGYSSTDSGGNWIKGTASGNSRCHFCASASVGYO 594  
 Db 535 PGKSMMAIGGTYRGAGYAGYSSTDSGGNWIKGTASGNSRCHFCASASVGYO 590

RESULT 11  
 Q9JPR8 ID Q9JPR8 PRELIMINARY; PRT; 599 AA.  
 AC Q9JPR8;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
 GN GNA992 OR NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

```
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
  Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  Moxon E.R., Grandi G., Rappuoli R.;
RA "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF157608; AAK68869.1; -.
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match          91.5%; Score 2762.5; DB 2; Length 599;
Best Local Similarity 91.7%; Pred. No. 5.9e-108;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDL 59
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDEDEEL 60
Qy 60 EPVORTAVVLSFRSDKGGTGEKVEDTSNMGVYDCKGVLTAGVITLTKAGNLIKIKO--- 116
Db 61 EPVYRSALVQLFMIDKGGNGENESTGIGWSIYYDNHTLHGAVITLTKAGNLIKIKQNTN 120
Qy 117 -NTNENTNASSFTYSLKKDLTDLTSVTEKLSFSAANKVNITSDTKGLNFAKKTATNG 175
Db 121 KNTNENTNDSFTYSLKKDLTDLTSVTEKLSFGANKVNITSDTKGLNFAKKTATNG 180
Qy 176 DTTVHLNGIGSTLPTDITLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 235
Db 181 DTTVHLNGIGSTLPTDITLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 240
Qy 236 ASDNVDFVRYDVTVEFLSADTKTTTVNVESKDKGKRTVEKIGAKTSVIKEDGKLVTKGD 295
Db 241 ASDNVDFVHTYDVTVEFLSADTKTTTVNVESKDKGKRTVEKIGAKTSVIKEDGKLVTKGK 300
Qy 296 KGENDSTDKGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEVTSGTNVTFSAG 355
Db 301 KGENGSTDEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEVTSGTNVTFSAG 360
Qy 356 KGTATVSKDDQGNITVYDYNVDALNVQLNSGNWLDLSKAVAGSSGKVISGNVSPSK 415
Db 361 KGTATVSKDDQGNITVKYDYNVDALNVQLNSGNWLDLSKAVAGSSGKVISGNVSPSK 420
Qy 416 GKMDETVINAGNNIEITRNKNDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475
Db 421 GKMDETVINAGNNIEITRNKNDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480
Qy 476 KDANKPVRITNVPAGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIATAGLVQ 535
Db 481 KDANKPVRITNVPAGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIATAGLVQ 540
Qy 536 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594
Db 541 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 599

RESULT 12
```

```
Q9JPS7
ID Q9JPS7 PRELIMINARY; PRT; 591 AA.
AC Q9JPS7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
  Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  Moxon E.R., Grandi G., Rappuoli R.;
RA "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226366; AAF42515.1; -.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;
```

```
Query Match          91.4%; Score 2758.5; DB 2; Length 591;
Best Local Similarity 92.3%; Pred. No. 8.5e-108;
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;
```

```
Qy 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVETAVLATLLFATVQASANNEEEDL 60
Qy 58 YLEPVQRTAVVLSFRSDKGGTGEKE-VTEDSNMGVYDCKGVLTAGVITLTKAGNLIKIKO 116
Db 61 YLDPVQRTAVVLIYNSDKGGTGEKEVEENSDWAVYENKGVLTARETLTKAGNLIKIKO 120
Qy 117 NTNENTNASSFTYSLKKDLTDLTSVTEKLSFSAANKVNITSDTKGLNFAKKTATNGD 176
Db 121 -----NGTNTFTYSLKKDLTDLTSVTEKLSFSAANKVNITSDTKGLNFAKKTATNGD 174
Qy 177 TTVHLNGIGSTLPTDITLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236
Db 175 TTVHLNGIGSTLPTDITLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 234
Qy 237 SDNVDFVRYDVTVEFLSADTKTTTVNVESKDKGKRTVEKIGAKTSVIKEDGKLVTKGDK 296
Db 235 SDNVDFVRYDVTVEFLSADTKTTTVNVESKDKGKRTVEKIGAKTSVIKEDGKLVTKGDK 294
Qy 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEVTSGTNVTFSAGK 356
Db 295 GENGSTDEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEVTSGTNVTFSAGK 354
Qy 357 GTTATVSKDDQGNITVYDYNVDALNVQLNSGNWLDLSKAVAGSSGKVISGNVSPSK 416
Db 355 GTTATVSKDDQGNITVYDYNVDALNVQLNSGNWLDLSKAVAGSSGKVISGNVSPSK 414
Qy 417 KMDETVINAGNNIEITRNKNDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 415 KMDETVINAGNNIEITRNKNDIATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
Qy 477 DANKPVRITNVPAGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIATAGLVQA 536
Db 474 KDNKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIATAGLVQA 533
Qy 537 YLPKSKMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594
Db 534 YLPKSKMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 591
```

4:

QY	176	DTTVHLNGIGSTLDTLLNGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTT	233
Db	175	DTTVHLNGIGSTLDTLLNGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTT	234
QY	236	ASDNVDFVRTYDFVEFLSADTKTTTNNVNESKONGKRTVEKIGAKTSVIEKEDGKLVTKGD	295
Db	235	ASDNVDFVRTYDFVEFLSADTKTTTNNVNESKONGKRTVEKIGAKTSVIEKEDGKLVTKGD	294
QY	296	KGENSDSTDKEGVLTAKEVIDAVNKAQRMKTTTTANGOTGQADKFETVTSNTNVTFSAG	355
Db	295	KGENSGSTDBEGVLTAKEVIDAVNKAQRMKTTTTANGOTGQADKFETVTSNTNVTFSAG	354
QY	356	KGTTATVSKDDQGNITVMYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVIISGNVSPSK	415
Db	355	KGTTATVSKDDQGNITVMYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVIISGNVSPSK	414
QY	416	GKMDETVNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDDEGALNVGS	475
Db	415	GKMDETVNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDDEGALNVGS	473
QY	476	KDANKPVRTINAPGVKEGDVTNVAOLKGVAQNLNHHIDNVGDNARAGITAOIAITAGLVQ	535
Db	474	KKONKPVRTINAPGVKEGDVTNVAOLKGVAQNLNHHIDNVGDNARAGITAOIAITAGLVQ	533
QY	536	AYLPFGKSMAAIGGTTVRGEAGYAGIYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	594
Db	534	AYLPFGKSMAAIGGTTVRGEAGYAGIYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	592
RESULT 15			
Q93QY3			
ID	Q93QY3	PRELIMINARY;	PRT; 591 AA.
AC	Q93QY3;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	NHHA OUTER MEMBRANE PROTEIN.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxId=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EG329;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis.";		
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.		
RL	EMBL; AF157606; AAK68867.1; -.		
SR	SEQUENCE 591 AA; 62048 MW; CQDC600798859C65 CIRC64;		





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:24:43 ; Search time 58.77 Seconds  
(without alignments)  
1122.645 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MKKIYRIWNSALNAWVVS.....TASGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 15

Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.\*  
6: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT.\*  
7: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT.\*  
8: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.\*  
15: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.\*  
16: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.\*  
17: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.\*  
18: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	100.0	594	20 AAY23740	A surface protein
2	594	100.0	594	21 AAY57044	BASB029 amino acid
3	594	100.0	594	22 AAU06174	N. meningitidis EG
4	161	27.1	407	22 AAU06184	N. meningitidis PM
5	161	27.1	433	22 AAU06185	N. meningitidis PM
6	161	27.1	502	22 AAU06186	N. meningitidis PM
7	161	27.1	512	22 AAU06182	N. meningitidis PM
8	161	27.1	591	20 AAY27202	Amino acid sequenc
9	161	27.1	591	20 AAY23741	A surface protein
10	161	27.1	591	20 AAY23746	A surface protein
11	161	27.1	591	21 AAY57045	BASB029 amino acid

us-09-700-293-2.oligo.rag

Page 1

12 161 27.1 591 22 AAU06171

13 161 27.1 591 22 AAU06175

14 161 27.1 592 20 AAY23737

15 138 23.2 513 22 AAU06183

16 138 23.2 589 20 AAY23745

17 138 23.2 589 20 AAU06173

18 138 23.2 592 20 AAY23744

19 138 23.2 592 22 AAU06172

20 138 23.2 598 20 AAY23738

21 138 23.2 598 20 AAY23742

22 138 23.2 598 22 AAU06177

23 138 23.2 598 22 AAU06178

24 127 21.4 592 22 AAY27203

25 127 21.4 592 22 AAU06180

26 98 16.5 245 20 AAY27201

27 94 15.8 599 20 AAY23743

28 94 15.8 599 22 AAU06176

29 93 15.7 594 20 AAY23739

30 93 15.7 594 22 AAU06179

31 82 13.8 116 21 AAB37832

32 72 12.1 72 21 AAB37830

33 59 9.9 604 22 AAU06181

34 43 7.2 53 21 AAB37828

35 32 5.4 56 21 AAB37827

36 23 3.9 1098 17 AAR99392

37 22 3.7 2353 17 AAR99393

38 22 3.7 2411 21 AAB23860

39 20 3.4 20 21 AAB37831

40 19 3.2 19 21 AAB51546

41 19 3.2 19 21 AAB51547

42 18 3.0 1004 21 AAB23857

43 17 2.9 17 21 AAB37818

44 17 2.9 1094 21 AAB23858

45 16 2.7 16 21 AAB37819

46 16 2.7 16 21 AAB37829

47 15 2.5 15 21 AAB37822

48 15 2.5 15 21 AAB37825

49 15 2.5 23 21 AAB37824

RESULT 1

AA23740

ID AAY23740 standard; Protein; 594 AA.

XX AC AAY23740;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;

XX KW immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN WO9931132-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85792.

ALIGNMENTS

AA23740

ID AAY23740 standard; Protein; 594 AA.

XX AC AAY23740;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;

XX KW immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN WO9931132-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85792.

```

XX  Neisseria meningitidis surface proteins useful for treating N.
PT  meningitidis infections
XX
XX  Claim 1; Page 100-101; 132pp; English.
XX
CC  The present sequence represents a surface protein of Neisseria
CC  meningitidis which is approximately 62 kDa. The N. meningitidis
CC  surface glycoproteins, nucleic acids, the primers and optionally
CC  a thermostable polymerase, or antibodies are useful in a kit for
CC  the detection or diagnosis of N. meningitidis infection in humans.
CC  The N. meningitidis surface glycoproteins can also be used to
CC  prevent or treat N. meningitidis infection in humans, especially
CC  in the form of vaccines. The proteins and antibodies can also
CC  be used to identify immunoreactive peptides.
XX
XX  Sequence 594 AA;

Query Match      100.0%; Score 594; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
DB  1 mnkiyriwnsalnawavseltrnhtkrasatvatvatltilfatvgastdddddyle 60
QY  61 PVQRTAVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTAGTITLKAGDNLIKQNTNE 120
DB  61 pvqrtavlsfrsdkegtgektevdsnmgvyfdkkgvltagtitlkagdnlikkqntne 120
QY  121 NTWASSFTYSLKKDLTDLTSVGTETKLSFNSANSKNVITSDTKGLNFAKKTAEETNGDTTVH 180
DB  121 ntwnassftysslkkltdltsvgtetklsfnsansknvitsdtkglnfakktaeetngdttvh 180
QY  181 LNIIGSTLTDLLNTGATTNVTNDNVDDEKRAASVKDVLNAGNIIKGVKPGTASDNV 240
DB  181 lngigstltdllntgattnvtndnvddekraasvkdvlnagniikgvkpgtasdnv 240
QY  241 DFVRTYDTEFLSADTKTTNVNVEKDKGRTEVKIGAKTSVIEKDKGLVTGDKGEND 300
DB  241 dfvrtdydteflsadtkttnvnvesdkgrtevkigaktsviekdkglvtgdkgend 300
QY  301 SSTDKGGLVTAKEVIDAVNKAQWKRMTTANGOTGADKPEFTVTSCTNVTFSKGKTTA 360
DB  301 sstdkzglvtakevidavnkaqwmkrmttangotgadkpeftvtsctnvtfskgkttta 360
QY  361 TVSKDQGNITVWYDVNVDGNALNVQLQNSGNWLDKAVAGSGKIVSGNVSPSKGMDE 420
DB  361 tvskdqqnitvwydvnvdgnalnvqlqnsqgnwldskavagsgkivsgnvspskgmde 420
QY  421 TVNINAGNIIETRNKKNIDITATSMTPQFSVSLGAGADAPTLVSVDDEGALNVGSKDANK 480
DB  421 tvninagnnieitrngknidiatstmpqfssvslgagadaptlvsddegalnvgskdank 480
QY  481 PVRITNAPGVKRGSDVTNVAOLKGAQNLNNHIDNDGNARAGIAQAIATAGLVQAYLPG 540
DB  481 pvrtnapgvkrgsdvtnvaoalkgaqnlnnhiddndgnaragiaqaiataglvqaylpg 540
QY  541 KSMMAIGGTYRGEAGYAGYSSISDGNWIKGTASGNSRGRHFGASASVGYQW 594
DB  541 ksmmailggtyrgeagyaigyssisdgnwikgtasgnsrgrhfgasasvgyqw 594

RESULT 2
AAV57044
ID  AAV57044 standard; Protein; 594 AA.
XX
AC  AAV57044;
XX
DT  21-FEB-2000 (first entry)
XX
DE  BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

```

```

XX  BASB029; Neisseria meningitidis; surface fibrill protein; HSF; diagnosis;
KW  infection; treatment; prevent; antibacterial drug.
XX
XX  Neisseria meningitidis.
OS
XX
XX  Key      Location/Qualifiers
FT  Misc-difference 104
FT  /note= "Encoded by AATC"
XX
XX  W09958683-A2.
PN
XX
XX  18-NOV-1999.
PD
XX
XX  07-MAY-1999; 99WO-EP03255.
PF
XX
XX  13-MAY-1998; 98GB-0010276.
PR
XX
XX  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
FA
XX
XX  Ruelle J;
PI
XX
XX  WPI; 2000-053103/04.
DR
XX
XX  N-PSDB; AAZ39864.
DR
XX
XX  New polypeptide from neisseria meningitidis useful for diagnosis,
PT  treatment or prevention of bacterial infections in mammal
XX
XX  Claim 4; Fig 2; 74pp; English.
XX
XX  This is the Neisseria meningitidis BASB029 amino acid sequence from
CC  serogroup B strain ATCC13090. The BASB029 protein is homologous to the
CC  Haemophilus influenzae surface fibril (HSF) protein. The invention
CC  relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC  polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
CC  BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC  meningitidis infection in a mammal. Compositions containing BASB029
CC  polynucleotides and polypeptides are useful for generating an immune
CC  response in an animal. A therapeutic composition comprising an antibody
CC  directed against BASB029 is useful in treating humans with Neisseria
CC  meningitidis disease. The polynucleotide is useful in the diagnosis of
CC  the stage of infection, type of infection, susceptibility to an
CC  infection which results from increased or decreased expression of the
CC  polynucleotide, and for therapeutic or prophylactic purposes,
CC  particularly genetic immunisation. Antibodies against BASB029
CC  polynucleotides and polypeptides are also useful for treating infections
CC  particularly bacterial infections. The protein is useful in the
CC  screening and development of antibacterial drugs. Fused recombinant
CC  protein is useful for the stimulation of the immune system of an organism
CC  receiving the protein.
XX
XX  Sequence 594 AA;

Query Match      100.0%; Score 594; DB 21; Length 594;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
DB  1 mnkiyriwnsalnawavseltrnhtkrasatvatvatltilfatvgastdddddyle 60
QY  61 PVQRTAVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTAGTITLKAGDNLIKQNTNE 120
DB  61 pvqrtavlsfrsdkegtgektevdsnmgvyfdkkgvltagtitlkagdnlikkqntne 120
QY  121 NTWASSFTYSLKKDLTDLTSVGTETKLSFNSANSKNVITSDTKGLNFAKKTAEETNGDTTVH 180
DB  121 ntwnassftysslkkltdltsvgtetklsfnsansknvitsdtkglnfakktaeetngdttvh 180
QY  181 LNIIGSTLTDLLNTGATTNVTNDNVDDEKRAASVKDVLNAGNIIKGVKPGTASDNV 240
DB  181 lngigstltdllntgattnvtndnvddekraasvkdvlnagniikgvkpgtasdnv 240

```

QY 241 DFVRTYDTVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIREKDGKLVTKDKGEND 300  
 DB 241 dfvrtvdtveflsadtktttvneskdngkrtvkgaktsvirekdglvtgdkgend 300  
 QY 301 SSTDKGEGLVTAKEVIDAVNAGWRMKTTTANGQTGQADKFETVTSGTNVTTFASGKGTTA 360  
 DB 301 sstdkgeglvtakevidavnagwrmttttanggtgqadkfetvtsgtntvtfasgkgtta 360  
 QY 361 TVSKDDQGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNSVSPSKGKMD 420  
 DB 361 tvskddqgnitvmvdydvngdnlvnlqnswnldskavagssgkvisgnsvspsgkmd 420  
 QY 421 TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANK 480  
 DB 421 tvninagnieitrngknidiatsmtpqfssvslgagadaptlsvddgalnvsgkdank 480  
 QY 481 PVRITNAPGVKEGDTNVAQLKGVAQNLNHIDNVGDNARAGTAQATATAGLVQAYLPG 540  
 DB 481 pvrntnvgpvgkedtnvaqlkgvaqnlhndnvdgdnaragtaqataglvqaylpg 540  
 QY 541 KSMMAIGGTYRGAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
 DB 541 ksmmaiggtyrgagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 3

AAU06174

ID AAU06174 standard; Protein: 594 AA.

XX AC AAU06174;

XX DT

XX 24-OCT-2001 (first entry)

XX N. meningitidis EG327 surface antigen Nhha polypeptide sequence.  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 KW Neisseria meningitidis strain EG327.

XX Key Location/Qualifiers  
 XX Region 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..104  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 105..116  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 117..126  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT 127..190  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 191..212  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 213..231  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 232..238  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 239..594  
 FT /label= C5  
 FT /note= "Conserved region 5"

XX WO20015182-A1.

XX PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

XX WPI: 2001-488774/53.

XX N-PSDB: AAS09164.

XX New Nhha surface antigen polypeptides and polynucleotides from

XX Neisseria meningitidis, useful in producing vaccines for treating or

XX preventing broad spectrum of Neisseria meningitidis -

XX Claim 9; Fig 1; 9lpp; English.

XX The present invention relates to the isolation of novel Neisseria

XX meningitidis mutant polypeptides of the surface antigen Nhha

XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

XX characterised by deletions of non-conserved amino acids, particularly

XX the deletion of variable regions. The deletion mutants are useful in

XX diagnostics, therapeutic and prophylactic vaccines against a broader

XX spectrum of N. meningitidis, and in designing and/or screening of

XX medicaments. The mutant proteins when used as a vaccine can effectively

XX immunise against a broader spectrum of N. meningitidis strains than

XX The present sequence representing the wild type surface antigen Nhha

XX from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences

XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

XX the present invention.

XX Sequence 594 AA;

Query Match 100.0%; Score 594; DB 22; Length 594;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVCASTDDDDLYLE 60

DB 1 mnklyriiwnalnawavseltrnhtkrasatvatavtatlflfatvcastdddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFQKGVLTAGTITLAKAGDLKIKQNTNE 120

DB 61 pvqrtavvlsfrsdkegtgekevtesnwgvfyfkgvltagtitlkgadnlkikqntne 120

QY 121 NTNASSFTYSLKDLTDLTTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKKTATNGDTTVH 180

DB 121 ntnassftyislkdltdltsvgteklsfsansknvntsdtkglnfakktatngdttvh 180

QY 181 LINGIGSTLTDLTLLNTGATTNVTNDNVTDEKKRAASVDVLNAGWNIVKVPKGTASDNV 240

DB 181 lngigstltdlntgattnvtdnvtdekkraasvdkvlnagwnivkvpkgtasdnv 240

QY 241 DFVRTYDTVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIREKDGKLVTKDKGEND 300

DB 241 dfvrtvdtveflsadtktttvneskdngkrtvkgaktsvirekdglvtgdkgend 300

QY 301 SSTDKGEGLVTAKEVIDAVNAGWRMKTTTANGQTGQADKFETVTSGTNVTTFASGKGTTA 360

DB 301 sstdkgeglvtakevidavnagwrmtttanggtgqadkfetvtsgtntvtfasgkgtta 360

QY 361 TVSKDDQGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNSVSPSKGKMD 420

DB 361 tvskddqgnitvmvdydvngdnlvnlqnswnldskavagssgkvisgnsvspsgkmd 420

QY 421 TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANK 480

DB 421 tvninagnieitrngknidiatsmtpqfssvslgagadaptlsvddgalnvsgkdank 480

QY 481 PVRITNAPGVKEGDTNVAQLKGVAQNLNHIDNVGDNARAGTAQATATAGLVQAYLPG 540

DB 481 pvrntnvgpvgkedtnvaqlkgvaqnlhndnvdgdnaragtaqataglvqaylpg 540

```
Db 481 pvrtnvpgvkgdvtvnaqlkgvaqnlmnhidvndgnaragisqaiataglvqaylpg 540
QY 541 KSMWATGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHPGASASVGYQW 594
Db 541 ksmma199gtyrgeagyaigysisddgnwilkgtasgnrghnfgasasvgyqw 594

RESULT 4
AAU06184
ID AAU06184 standard; Protein; 407 AA.
XX
AC AAU06184;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #2.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
XX
FH Key Location/Qualifiers
FT Peptide 1..51
FT /label= Signal_peptide
FT Protein 52..407
FT /label= Mature_Nhha_deletion_mutant_#2
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX
XX N-PSDB; AAS09174.
XX
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 7; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence represents N. meningitidis strain PMC21 surface
XX antigen Nhha deletion mutant #2.
XX
XX Sequence 407 AA;

Query Match 27.1%; Score 161; DB 22; Length 407;
Best Local Similarity 100.0%; Pred. No. 1..4e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLYTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSGTNTVFASGKGTATVSKD 365
```

```
Db 120 geglvtakevldavnkagrmktttangotgqadkfetvtsgtntvfaskgttatvskd 179
QY 366 DQGNITVMDYVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKGKMDFTVIN 425
Db 180 dognitvmdydvngdnlvngqlnsgwnldskavagssgkvisgnvpskgkmdetvni 239
QY 426 AGNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVD 466
Db 240 agnieitrngknidiatsmtptqfssvslgagadapltlsvd 280

RESULT 5
AAU06185
ID AAU06185 standard; Protein; 433 AA.
XX
AC AAU06185;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #3.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
XX
FH Key Location/Qualifiers
FT Peptide 1..51
FT /label= Signal_peptide
FT Protein 52..433
FT /label= Mature_Nhha_deletion_mutant_#3
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX
XX N-PSDB; AAS09175.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 8; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence represents N. meningitidis strain PMC21 surface
XX antigen Nhha deletion mutant #3.
XX
XX Sequence 433 AA;
```

CC	antigen Nhha deletion mutant #4.
XX	
SQ	Sequence 502 AA;
	Query Match 27.1%; Score 161; DB 22; Length 502;
	Best Local Similarity 100.0%; Pred. No. 1.3e-149;
	Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	306 GEGIVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSGTNVTFASGKGTATVSKD 365 
Db	215 gegltakevidavnkagwrmtttangqtgqadkfetvtsgtnvtfasgkgtatvskd 274 
QY	366 DQGNIITVMYDVNVDGALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKGMDETWNIN 425 
Db	275 dqgnitvm ydvngdalnv nqlnsgw nldskavags gkv isgnv spskgm detwnin 334 
QY	426 AGNNIEITRNGKNIDIASTMPQFSSVSLGAGADAPTLSDV 466 
Db	335 agnnieitrngknidiatstmpqfssvslgagadaptlsvd 375 
RESULT	7
AAU06182	
ID	AAU06182 standard; Protein; 512 AA.
XX	
AC	AAU06182;
DT	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis PMC21 Nhha deletion mutant #1.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW	mutant; mutein.
XX	
OS	Neisseria meningitidis strain PMC21.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..51
FT	/label= Signal_peptide
FT	Protein 52..512
FT	/label= Mature_Nhha_deletion_mutant.#1
FT	/note= "Predicted mature protein, specifically claimed in claim 12"
XX	
PN	WC200155182-A1.
XX	
PD	02-AUG-2001.
XX	
PF	25-JAN-2001; 2001WO-AU000069.
XX	
PR	25-JAN-2000; 2000US-0177917.
XX	
PA	(UYQU ) UNIV QUEENSLAND.
XX	
PI	Peak IRA, Jennings MP;
XX	
DR	WPI: 2001-488774/53.
DR	N-PSDB: AAS09172.
XX	
PT	New Nhha surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 12; Fig 5; 9ipp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhha
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhma deletion mutant #1.

XX SQ Sequence 512 AA;

Query Match 27.1%; Score 161; DB 22; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-149;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLYTAKEVIDAVNKGWRMKTTHANGQTQADKFETVTSCTNVTTFASGKGTATVSKD 365  
 |||||  
 Db 225 geglytakevidavnkagwrmtttangtqgqdkfetsgtntvtfasgkgtatvskd 284  
 |||||  
 QY 366 DQGNITVMDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGRKMDVTNIN 425  
 |||||  
 Db 285 dggnitvmdyvnvgdalinvnqlnsgwnldskavagssgkvvisgnvspsgkmdetvnl 344  
 |||||  
 QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
 |||||  
 Db 345 agnnieitrngknidiatsmtpqfssvslgagadaptilsvd 385

# RESULT 8

AAV27202  
 ID AAY27202 standard; Protein; 591 AA.

XX AC AAY27202;

XX DT 24-SEP-1999 (first entry)

XX DE Amino acid sequence of N. meningitidis protein ORF40-1.

XX KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
 XX bacterial infection; treatment.

XX OS Neisseria meningitidis.

XX PN W09936544-A2.

XX PD 22-JUL-1999.

XX PF 14-JAN-1999; 99WO-IB00103.

XX PR 09-OCT-1998; 98GB-0022143.

XX PR 14-JAN-1998; 98GB-0000760.

XX PR 01-SEP-1998; 98GB-0019015.

XX PA (CHIR-) CHIRON SPA.

XX PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;

XX DR WPI; 1999-444400/37.

XX DR N-PSDB; AAX99124.

XX PT New protein and its nucleotide sequence, useful in vaccines or  
 XX diagnostic compositions for treating and/or preventing Neisseria  
 XX meningitidis infections

XX PS Claim 1; Page 62; 123pp; English.

XX CC The invention provides proteins (AAY27201-245) from Neisseria  
 CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
 CC encoding the proteins. Compositions comprising the protein, nucleic acid  
 CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
 CC vaccine composition or a diagnostic composition. The composition is also  
 CC useful for treating or preventing an infection due to Neisseria  
 CC bacteria, especially Neisseria meningitidis.

XX

SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLYTAKEVIDAVNKGWRMKTTHANGQTQADKFETVTSCTNVTTFASGKGTATVSKD 365  
 |||||  
 Db 304 geglytakevidavnkagwrmtttangtqgqdkfetsgtntvtfasgkgtatvskd 363  
 |||||  
 QY 366 DQGNITVMDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGRKMDVTNIN 425  
 |||||  
 Db 364 dggnitvmdyvnvgdalinvnqlnsgwnldskavagssgkvvisgnvspsgkmdetvnl 423  
 |||||  
 QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
 |||||  
 Db 424 agnnieitrngknidiatsmtpqfssvslgagadaptilsvd 464

# RESULT 9

AAV23741

ID AAY23741 standard; Protein; 591 AA.

XX AC AAY23741;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;  
 XX immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN W09931132-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX DR WPI; 1999-418754/35.

XX DR N-PSDB; AAX85793.

XX PT Neisseria meningitidis surface proteins useful for treating N.  
 XX meningitidis infections

XX PS Claim 1; Page 104-106; 132pp; English.

XX CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEFVTSGTNTVFASGKGTATVSKD 365  
Dy 304 geglvtakevidavnkagwrkmktttangtqtgqadkfetvtsgtntvfaskgttatvskd 363  
Qy 366 DQGNITVMYDYNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNIN 425  
Dy 364 dqgnitvmynvvgdalinvgdlnqnsqwnldskavagssgkvisgnvspskgkmdetvnnin 423  
Qy 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVD 466  
Dy 424 agnnieitrngkniidiatsmtpqfssvslgagadaptilsvd 464  
RESULT 10  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
AC AAY23746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;  
Query Match 27.1%; Score 161; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEFVTSGTNTVFASGKGTATVSKD 365  
Dy 304 geglvtakevidavnkagwrkmktttangtqtgqadkfetvtsgtntvfaskgttatvskd 363  
Qy 366 DQGNITVMYDYNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNIN 425  
Dy 364 dqgnitvmynvvgdalinvgdlnqnsqwnldskavagssgkvisgnvspskgkmdetvnnin 423

Qy 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVD 466  
Dy 424 agnnieitrngkniidiatsmtpqfssvslgagadaptilsvd 464  
RESULT 11  
AAY57045  
ID AAY57045 standard; Protein; 591 AA.  
XX  
AC AAY57045;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 90 /note= "Encoded by AAT"  
FT Misc-difference 92 /note= "Encoded by CAT"  
FT Misc-difference 98 /note= "Encoded by AAC"  
FT Misc-difference 108 /note= "Encoded by AATC"  
FT Misc-difference 123 /note= "Encoded by ACA"  
FT Misc-difference 269 /note= "Encoded by AAA"  
FT Misc-difference 389 /note= "Encoded by CGT"  
XX  
PN WO9958683-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Ruelle J;  
XX  
DR WPI; 2000-053103/04.  
DR N-PSDB; AAZ39865.  
XX  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Neisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections





Qy	366	DOGNITVMYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKMDETVNN	425
Db	364	dqgnitvmydvnvgdalnvnlqngwnldskavagssgkvisgnvpskgkmdetvnn	423
Qy	426	AGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDV	466
Db	424	agnieitrngknidiatstmpqfssvslgagadaptsldv	464
RESULT 14			
AA	AY23737		
ID	AA23737 standard; Protein; 592 AA.		
XX	AC	AY23737;	
XX	AC		
DT	08-SEP-1999	(first entry)	
XX			
DE	A surface protein of Neisseria meningitidis.		
XX			
KW	Surface protein; surface glycoprotein; infection; vaccine;		
KW	immunoreactive peptide.		
XX			
OS	Neisseria meningitidis.		
XX			
PN	WO9931132-A1.		
XX			
PD	24-JUN-1999.		
XX			
PF	14-DEC-1998; 98WO-AU01031.		
XX			
PR	12-DEC-1997; 97GB-0026398.		
XX			
PA	(ISIS-) ISIS INNOVATION LTD.		
PA	(UYQU ) UNIV QUEENSLAND.		
XX			
PI	Jennings MP, Moxon ER, Peak IRA;		
XX			
DR	WPI: 1999-418754/35.		
DR	N-PSDB; AAX85788.		
XX			
PT	Neisseria meningitidis surface proteins useful for treating N.		
PT	meningitidis infections		
XX			
PS	Claim 1; Page 86-87; 132pp; English.		
XX			
CC	The present sequence represents a surface protein of Neisseria		
CC	meningitidis which is approximately 62 kDa. The N. meningitidis		
CC	surface glycoproteins, nucleic acids, the primers and optionally		
CC	a thermostable polymerase, or antibodies are useful in a kit for		
CC	the detection or diagnosis of N. meningitidis infection in humans.		
CC	The N. meningitidis surface glycoproteins can also be used to		
CC	prevent or treat N. meningitidis infection in humans, especially		
CC	in the form of vaccines. The proteins and antibodies can also		
CC	be used to identify immunoreactive peptides.		
XX			
SQ	Sequence 592 AA;		
Query Match 27.1%; Score 161; DB 20; Length 592;			
Best Local Similarity 100.0%; Pred. No. 1.5e-149;			
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps			
Qy	306	GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKPFVTSNGTNVTFASGKGTATVSKD	355
Db	305	gegvlvtakevldavnkagwrmktttangqgqadkfvtvtsgntvtfasgkgtatvskd	364
Qy	366	DOGNITVMYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKMDETVNN	425
Db	365	dqgnitvmydvnvgdalnvnlqngwnldskavagssgkvisgnvpskgkmdetvnn	424
Qy	426	AGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDV	466

Db 353 rnkgnkdiatsmtpqfssvslgagadaptilsvddegalnvgskdankpvrtnvapgvke 412  
QY 494 GDVTNVAQLKGVAQNINN 511  
Db 413 gdvtlnvaqlkgvaqnlmn 430

Search completed: September 5, 2002, 10:31:59  
Job time: 436 sec

Db 425 agnnieitrngknidiatsmtpqfssvslgagadaptilsvd 465

RESULT 15  
AAU06183  
ID AAU06183 standard; Protein; 513 AA.  
XX AC AAU06183; ~  
XX DT 24-OCT-2001 (first entry)  
XX DE N. meningitidis H41 Nhha deletion mutant.  
XX DE Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
XX KW mutant; mutein.  
XX OS Neisseria meningitidis strain H41.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT 1..51  
XX FT /label= Signal\_peptide  
XX FT 52..513  
XX FT Protein  
XX FT /label= Mature\_Nhha\_deletion\_mutant  
XX FT /note= Predicted mature protein, specifically  
XX FT claimed in claim 12"  
XX PN WO200155182-A1.  
XX PD 02-AUG-2001.  
XX PF 25-JAN-2001; 2001WO-AU00069.  
XX PR 25-JAN-2000; 2000US-0177917.  
XX PA (UYQU ) UNIV QUEENSLAND.  
XX PI Peak IRA, Jennings MP;  
XX PT WPI; 2001-488774/53.  
XX DR N-PSDB; AAS09173.  
XX PT New Nhha surface antigen polypeptides and polynucleotides from  
XX PT Neisseria meningitidis, useful in producing vaccines for treating or  
XX PT preventing broad spectrum of Neisseria meningitidis -  
XX PS Claim 12; Fig 6; 91pp; English.  
XX CC The present invention relates to the isolation of novel Neisseria  
XX CC meningitidis mutant polypeptides of the surface antigen Nhha  
XX CC (AAU06182-AAU06186). The identified or mutant Nhha polypeptides are  
XX CC characterised by deletion of non-conserved amino acids, particularly  
XX CC the deletion of variable regions. The deletion mutants are useful in  
XX CC diagnostic, therapeutic and prophylactic vaccines against a broader  
XX CC spectrum of N. meningitidis, and in designing and/or screening of  
XX CC mutants. The mutant proteins when used as a vaccine can effectively  
XX CC immunise against a broader spectrum of N. meningitidis strains than  
XX CC would be expected from a corresponding wild-type surface antigen.  
XX CC The present sequence represents N. meningitidis strain H41 surface  
XX CC antigen Nhha deletion mutant.  
XX SQ Sequence 513 AA;

Query Match 23.2%; Score 138; DB 22; Length 513;  
Best Local Similarity 100.0%; Pred. No. 5.9e-127;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVQNLQNSGNLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNNIET 433  
Db 293 ydvnvgdalnvnqignsgwnldskavagsgkvisgnvpsksgkmdetvnnagnnieit 352  
QY 434 RNMKNIDIATSMTPQFSSVSLGAGADAPTLISVDDEGALNVGSKDANKPVRITNVAFCVKE 493



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:28:13 ; Search time 25.6 Seconds  
(without alignments)  
566.750 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TAGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 15

Total number of hits satisfying chosen parameters: 41

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	594	100.0	594	4	US-09-377-155-9
2	594	100.0	594	4	US-09-669-974-9
3	161	27.1	591	4	US-09-377-155-11
4	161	27.1	591	4	US-09-377-155-21
5	161	27.1	591	4	US-09-669-974-11
6	161	27.1	591	4	US-09-669-974-21
7	161	27.1	592	4	US-09-377-155-2
8	161	27.1	592	4	US-09-669-974-2
9	138	23.2	589	4	US-09-377-155-19
10	138	23.2	589	4	US-09-669-974-19
11	138	23.2	592	4	US-09-377-155-17
12	138	23.2	592	4	US-09-669-974-17
13	138	23.2	598	4	US-09-377-155-5
14	138	23.2	598	4	US-09-377-155-13
15	138	23.2	598	4	US-09-669-974-5
16	138	23.2	598	4	US-09-669-974-13
17	94	15.8	599	4	US-09-377-155-15
18	94	15.8	599	4	US-09-669-974-15
19	93	15.7	594	4	US-09-377-155-7
20	93	15.7	594	4	US-09-669-974-7
21	23	3.9	658	1	US-08-409-995-5
22	23	3.9	658	3	US-08-409-995-5
23	23	3.9	658	4	US-08-685-467-5
24	23	3.9	1098	1	US-08-913-942-5
25	23	3.9	1098	3	US-08-409-995-2
26	23	3.9	1098	4	US-08-685-467-2
27	23	3.9	1098	4	US-09-377-155-32
					US-08-913-942-2

28	23	3.9	1098	4	US-09-669-974-32	Sequence 32, Appl
29	23	3.9	1098	4	US-09-268-347-44	Sequence 44, Appl
30	22	3.7	1912	1	US-08-409-995-4	Sequence 4, Appl
31	22	3.7	1912	3	US-08-685-467-4	Sequence 4, Appl
32	22	3.7	2353	4	US-09-377-155-33	Sequence 33, Appl
33	22	3.7	2353	4	US-08-913-942-4	Sequence 4, Appl
34	22	3.7	2353	4	US-09-669-974-33	Sequence 33, Appl
35	22	3.7	2354	4	US-09-268-347-47	Sequence 47, Appl
36	22	3.7	2411	4	US-09-268-347-36	Sequence 36, Appl
37	20	3.4	607	1	US-08-409-995-6	Sequence 6, Appl
38	20	3.4	607	3	US-08-685-467-6	Sequence 6, Appl
39	20	3.4	607	4	US-08-913-942-6	Sequence 6, Appl
40	18	3.0	1004	4	US-09-268-347-30	Sequence 30, Appl
41	17	2.9	1094	4	US-09-268-347-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
; US-09-377-155-9

Query Match	100.0%	Score 594;	DB 4;	Length 594;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 594;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDLYLE	60		
Db 1	MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDLYLE	60		
Qy 61	PVQRTAVVLSFRSDEKTEGEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE	120		
Db 61	PVQRTAVVLSFRSDEKTEGEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE	120		
Qy 121	NTNASSFTYSLKKDLTDLTSVGTTEKLSFSANSKNVNIITSDTKLNFPAKTAETNGDTTVH	180		
Db 121	NTNASSFTYSLKKDLTDLTSVGTTEKLSFSANSKNVNIITSDTKLNFPAKTAETNGDTTVH	180		
Qy 181	LNGIGSTLDTLLNTGATNTVNDVNDDEKRAASVKDVLNAGWNKIGVKPCTTASDNV	240		
Db 181	LNGIGSTLDTLLNTGATNTVNDVNDDEKRAASVKDVLNAGWNKIGVKPCTTASDNV	240		
Qy 241	DEVRYIDVFEFLSADTKITTVNVESKDNKRTVEVIGAKTSVKEKDGKLVTKDKGEND	300		
Db 241	DEVRYIDVFEFLSADTKITTVNVESKDNKRTVEVIGAKTSVKEKDGKLVTKDKGEND	300		
Qy 301	SSTDKEGLVTAKEVIDAVNKAGWRMKTNTANGQTGOADKFETVTSGTNTVFASGKGTTA	360		
Db 301	SSTDKEGLVTAKEVIDAVNKAGWRMKTNTANGQTGOADKFETVTSGTNTVFASGKGTTA	360		
Qy 361	TVSKDDQGNITVMYDVNVGDALNVNLQNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDE	420		

```
Db 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKMD 420
QY 421 TVNINAGNIEITRNGKNIDATSWTQPFSSVSLGAGADAPTLSDVDDGALNVGSKDANK 480
Db 421 TVNINAGNIEITRNGKNIDATSWTQPFSSVSLGAGADAPTLSDVDDGALNVGSKDANK 480
QY 481 PVRITNAPGVKGGDVTVNAOLKGAQNLANNHIDNVGNARAGIAQAATATAGLVOAYLPG 540
Db 481 PVRITNAPGVKGGDVTVNAOLKGAQNLANNHIDNVGNARAGIAQAATATAGLVOAYLPG 540
QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 594
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 594

RESULT 2
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 100.0%; Score 594; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSNALNAWAVSELITNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60
Db 1 MNKIYRIIWSNALNAWAVSELITNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGKEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLIKQNTNE 120
Db 61 PVORTAVVLSFRSDKEGTGKEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLIKQNTNE 120
QY 121 NTNASSFTYSLUKDLTDLTSLVGTGTEKLSFSANSKNVNITSDTKGLNFAKKTAEITNGDPTVH 180
Db 121 NTNASSFTYSLUKDLTDLTSLVGTGTEKLSFSANSKNVNITSDTKGLNFAKKTAEITNGDPTVH 180
QY 181 LAGIGSTLDTLLNTGATNTVNDNVTDDEKRAASVKDVLNAGNINIKGVKPGTTASDNV 240
Db 181 LAGIGSTLDTLLNTGATNTVNDNVTDDEKRAASVKDVLNAGNINIKGVKPGTTASDNV 240
QY 241 DFVRTYDVTVEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVIREKDGKLVTKDKEGND 300
Db 241 DFVRTYDVTVEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVIREKDGKLVTKDKEGND 300
QY 301 SSTDKGEGVLTAKEVIDAVNKAQWRMKTITANGQTQADKFEVTSCTNVTFSAGKGTGA 360
Db 301 SSTDKGEGVLTAKEVIDAVNKAQWRMKTITANGQTQADKFEVTSCTNVTFSAGKGTGA 360
QY 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKMD 420
```

```
Db 361 TVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKMD 420
QY 421 TVNINAGNIEITRNGKNIDATSWTQPFSSVSLGAGADAPTLSDVDDGALNVGSKDANK 480
Db 421 TVNINAGNIEITRNGKNIDATSWTQPFSSVSLGAGADAPTLSDVDDGALNVGSKDANK 480
QY 481 PVRITNAPGVKGGDVTVNAOLKGAQNLANNHIDNVGNARAGIAQAATATAGLVOAYLPG 540
Db 481 PVRITNAPGVKGGDVTVNAOLKGAQNLANNHIDNVGNARAGIAQAATATAGLVOAYLPG 540
QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 594
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGYQW 594

RESULT 3
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11

Query Match 27.1%; Score 161; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3,3e+144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLYTAKEVIDAVNKAQWRMKTITANGQTQADKFEVTSCTNVTFSAGKGTATATVSKD 365
Db 304 GEGLYTAKEVIDAVNKAQWRMKTITANGQTQADKFEVTSCTNVTFSAGKGTATVSKD 363
QY 366 DQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 425
Db 364 DQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 423
QY 426 AGNIEITRNGKNIDATSWTQPFSSVSLGAGADAPTLSDV 466
Db 424 AGNIEITRNGKNIDATSWTQPFSSVSLGAGADAPTLSDV 464

RESULT 4
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
```

; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 27.1%; Score 161; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144; Indels 0; Gaps 0;  
Matches 161; Conservative 0; Mismatches 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 363  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNN 425  
|||||  
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNN 423  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
|||||  
Db 424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464

RESULT 5  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 27.1%; Score 161; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144; Indels 0; Gaps 0;  
Matches 161; Conservative 0; Mismatches 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 363  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNN 425  
|||||  
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNN 423  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
|||||  
Db 424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464

RESULT 6  
US-09-669-974-21  
; Sequence 21, Application US/09669974

; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 27.1%; Score 161; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144; Indels 0; Gaps 0;  
Matches 161; Conservative 0; Mismatches 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 363  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNN 425  
|||||  
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNN 423  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
|||||  
Db 424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464

RESULT 7  
US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 27.1%; Score 161; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144; Indels 0; Gaps 0;  
Matches 161; Conservative 0; Mismatches 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 365  
|||||  
Db 305 GEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 364

QY 366 DCGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIIN 425  
Db 365 DCGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIIN 424

QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
Db 425 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 465

## RESULT 8

US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 27.1%; Score 161; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRKMTTANGQTQADKFETVTSCTNVTFSAGKGTATYSKD 365  
Db 305 GEGLVTAKEVIDAVNKAGWRKMTTANGQTQADKFETVTSCTNVTFSAGKGTATYSKD 364

QY 366 DCGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIIN 425  
Db 365 DCGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIIN 424

QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
Db 425 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 465

## RESULT 9

US-09-377-155-19  
; Sequence 19, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19

; LENGTH: 589  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-19

Query Match 23.2%; Score 138; DB 4; Length 589;  
Best Local Similarity 100.0%; Pred. No. 2e-122;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIINAGNIEIT 433  
Db 369 YDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIINAGNIEIT 428  
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRIITNVAPGVKE 493  
Db 429 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRIITNVAPGVKE 488

QY 494 GDVTNVAQLKGVAQNLNN 511  
Db 489 GDVTNVAQLKGVAQNLNN 506

## RESULT 10

US-09-669-974-19  
; Sequence 19, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 589  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-19

Query Match 23.2%; Score 138; DB 4; Length 589;  
Best Local Similarity 100.0%; Pred. No. 2e-122;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIINAGNIEIT 433  
Db 369 YDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIINAGNIEIT 428  
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRIITNVAPGVKE 493  
Db 429 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRIITNVAPGVKE 488

QY 494 GDVTNVAQLKGVAQNLNN 511  
Db 489 GDVTNVAQLKGVAQNLNN 506

## RESULT 11

US-09-377-155-17  
; Sequence 17, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm



	Query Match	23.2%	Score 138;	DB 4;	Length 592;
	Best Local Similarity	100.0%;	Pred. No. 2e-122;		
	Matches 138;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	374	YDVNVGDALNVQLQNSGWNLDSKAVAGSSKVTSGNVSPSKGRMDEVTNINAGNNIET	433		
Db	372	YDVNVGDALNVQLQNSGWNLDSKAVAGSSKVTSGNVSPSKGRMDEVTNINAGNNIET	431		
Qy	434	RNGNKDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITTNVAPGVKE	493		

	Query Match	23.2%	Score 138;	DB 4;	Length 598;
	Best Local Similarity	100.0%;	Pred. No. 2e-122;		
	Matches 138;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	374	YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVI	ISGNVSPSKGKMDETV	VNINAGNNIEIT	433
Db	378	YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVI	ISGNVSPSKGKMDETV	VNINAGNNIEIT	437
Qy	434	RNGKNIDIATSMTPQFSVSLGAGADAPT	LSVDDSEGALNVGSKDANKPVRIT	TVNAPGVKE	493
Db	438	RNGKNIDIATSMTPQFSVSLGAGADAPT	LSVDDSEGALNVGSKDANKPVRIT	TVNAPGVKE	497

```

RESULT 14
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

```

Query Match 23.28; Score 138; DB 4; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 2e-122;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 433  
 Db 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 437  
 Qy 434 RKGKNTDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
 Db 438 RKGKNTDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 497  
 Qy 494 GDTVNTVAQLKGVAQNLLN 511  
 Db 498 GDTVNTVAQLKGVAQNLLN 515

RESULT 15  
 US-09-669-974-5  
 ; Sequence 5, Application US/09669974  
 ; Patent No. 6333173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 06S064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/669, 974  
 ; CURRENT FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US 09/377,155  
 ; PRIOR FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 598  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria meningitidis  
 US-09-669-974-5

Query Match 23.28; Score 138; DB 4; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 2e-122;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 433  
 Db 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 437  
 Qy 434 RKGKNTDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
 Db 438 RKGKNTDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 497  
 Qy 494 GDTVNTVAQLKGVAQNLLN 511  
 Db 498 GDTVNTVAQLKGVAQNLLN 515

Search completed: September 5, 2002, 10:32:32  
 Job time: 259 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:29:43 ; Search time 33.86 Seconds  
(without alignments)  
1685.678 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 15

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 1000 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	27.1	591	2 G81133	adhesin NMB0992 [i
2	127	21.4	592	2 A81888	probable surface f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TET>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:32:38 ; Search time 19.19 Seconds  
(without alignments)  
1198.510 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNLSALNAWVVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
-----				

No matches found

Search completed: September 5, 2002, 10:39:36  
Job time: 418 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:32:03 ; Search time 55.9 Seconds  
(without alignments)  
1838.265 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TAGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 15

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query %		Length	DB	ID	Description		
		Match							
1	594	100.0	594	2	Q93QY4	Q93qy4	neisseria	m	
2	221	37.2	594	2	Q9JPI3	Q9jpi3	neisseria	m	
3	221	37.2	594	2	Q9JPS2	Q9jps2	neisseria	m	
4	221	37.2	595	2	Q9JPH0	Q9jph0	neisseria	m	
5	162	27.3	592	2	Q9JPS9	Q9jps9	neisseria	m	
6	162	27.3	598	2	Q9JPR7	Q9jpr7	neisseria	m	
7	162	27.3	599	2	Q9JPS8	Q9jps8	neisseria	m	
8	161	27.1	591	2	Q9JPS7	Q9jps7	neisseria	m	
9	161	27.1	591	2	Q93QY3	Q93qy3	neisseria	m	
10	161	27.1	591	16	Q9JRI8	Q9jri8	neisseria	m	
11	161	27.1	592	2	Q9AQF0	Q9aqf0	neisseria	m	
12	138	23.2	589	2	Q9JPI0	Q9jpi0	neisseria	m	
13	138	23.2	589	2	Q93QY1	Q93qy1	neisseria	m	
14	138	23.2	590	2	Q9JPS3	Q9jps3	neisseria	m	
15	138	23.2	592	2	Q93QY2	Q93qy2	neisseria	m	
16	138	23.2	598	2	Q9JPT0	Q9jpt0	neisseria	m	

17 138 23.2 598 2 Q9JPS0 Q9jps0 neisseria m  
18 138 23.2 598 2 Q93QY5 Q93qy5 neisseria m  
19 138 23.2 600 2 Q9JPS5 Q9jps5 neisseria m  
20 127 21.4 592 16 Q9JOW4 Q9jow4 neisseria m  
21 94 15.8 599 2 Q9JPS8 Q9jps8 neisseria m  
22 93 15.7 526 2 Q9JPS4 Q9jps4 neisseria m  
23 93 15.7 530 2 Q9JPS1 Q9jps1 neisseria m  
24 93 15.7 594 2 Q9JPH7 Q9jph7 neisseria m  
25 93 15.7 598 2 Q9JPR9 Q9jpr9 neisseria m  
26 93 15.7 600 2 Q9JPS6 Q9jps6 neisseria m  
27 23 3.9 1098 2 Q48152 Q48152 haemophilus  
28 22 3.7 2353 2 P71401 P71401 haemophilus

ALIGNMENTS

RESULT 1

Q93QY4 ID Q93QY4 PRELIMINARY; PRT; 594 AA.  
AC Q93QY4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG327;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157605; AAK68866.1; .  
SQ SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;

Query Match 100.0%; Score 594; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60  
Qy 61 PVQRTAVVLSFRSDEKGTGEKVTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
Db 61 PVQRTAVVLSFRSDEKGTGEKVTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
Qy 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFANSKNYITSDTKGLNFAKTAETNGDTTVH 180  
Db 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFANSKNYITSDTKGLNFAKTAETNGDTTVH 180  
Qy 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVSDVNLNAGWNIKGVKPGTTASDNV 240  
Db 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVSDVNLNAGWNIKGVKPGTTASDNV 240  
Qy 241 DFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEVKIGAKTSVIKEKDKLVTKGDKGND 300  
Db 241 DFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEVKIGAKTSVIKEKDKLVTKGDKGND 300  
Qy 301 SSTDKGGLVTAKEVIDAVNAGWEMKTTTANGQFGQADKFFETVTSCTNVTFASGKGTTA 360  
Db 301 SSTDKGGLVTAKEVIDAVNAGWEMKTTTANGQFGQADKFFETVTSCTNVTFASGKGTTA 360  
Qy 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNILDSKAVAGSSGVISGNVSPSKGKMD 420  
Db 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNILDSKAVAGSSGVISGNVSPSKGKMD 420  
Qy 421 TVNINAGNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLSVDEGALNVGSKDANK 480





Query Match		37.2%; Score 221; DB 2; Length 595;
Best Local Similarity		100.0%; Pred. No. 4e-204;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	374 YDNNVGDALNNQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNNAGNNEIT	433
Db	375 YDNNVGDALNNQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNNAGNNEIT	434
Qy	434 RGNKNIDIATSWTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVPAGVKE	493
Db	435 RGNKNIDIATSWTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVPAGVKE	494
Qy	494 GDVTNVAQLKQVAQNLNHNIDVGNRAGIAQAIAATAGLVOAYLPKSKMMAIGGTYRG	553
Db	495 GDVTNVAQLKQVAQNLNHNIDVGNRAGIAQAIAATAGLVOAYLPKSKMMAIGGTYRG	554
Qy	554 EAGYAIGYSSISDGGNLIKTASGNSRGHFGASASVGYQW	594
Db	555 EAGYAIGYSSISDGGNLIKTASGNSRGHFGASASVGYQW	595
RESULT 5		
Q9JPS9	SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;	
ID	PRELIMINARY; PRT; 592 AA.	
AC	Q9JPS9;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DE	OUTER MEMBRANE PROTEIN GNA992.	
GN	GNA992.	
OS	Neisseria meningitidis.	
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
OX	NCBI_TaxID=487;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=860800;	
RX	MEDLINE=20175756; PubMed=10710308;	
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,	
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,	
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,	
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	
RA	Moxon E.R., Grandi G., Rappuoli R.;	
RT	Identification of Vaccine Candidates Against Serogroup B	
RL	Meningococcus by Whole-Genome Sequencing.;	
DR	EMBL; AF226361; AAF42510.1; -.	
SQ	SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;	
Query Match		
Best Local Similarity 100.0%; Pred. No. 3e-147;		
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTSVTNVTASGKGTATVSKD	365
Db	304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTSVTNVTASGKGTATVSKD	363
Qy	366 DQGNITVMYDVGDNALNVQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNN	425
Db	364 DQGNITVMYDVGDNALNVQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNN	423
Qy	426 AGNNIETRNKNIDIATSWTPQFSSVSLGAGADAPTLSDVDD	467
Db	424 AGNNIETRNKNIDIATSWTPQFSSVSLGAGADAPTLSDVDD	465
RESULT 6		
Q9JPR7	SEQUENCE 598 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;	
ID	PRELIMINARY; PRT; 598 AA.	
AC	Q9JPR7;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	

DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	OUTER MEMBRANE PROTEIN GNA992.
GN	GNA992.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX	NCBI_TaxID=487;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SWZ107;
RX	MEDLINE=20175756; PubMed=10710308;
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA	Moxon E.R., Grandi G., Rappuoli R.;
RT	"Identification of Vaccine Candidates Against Serogroup B
RL	Meningococcus by Whole-Genome Sequencing.";
DR	EMBL; AF226385; AAF42534.1; -.
SQ	SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
Qy	306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTSVTNVTASGKGTATVSKD 365
Db	310 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTSVTNVTASGKGTATVSKD 369
Qy	366 DQGNITVMYDVGDNALNVQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNN 425
Db	370 DQGNITVMYDVGDNALNVQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNN 429
Qy	426 AGNNIETRNKNIDIATSWTPQFSSVSLGAGADAPTLSDVD 467
Db	430 AGNNIETRNKNIDIATSWTPQFSSVSLGAGADAPTLSDVD 471
RESULT 7	
Q9JPS8	SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;
ID	PRELIMINARY; PRT; 599 AA.
AC	Q9JPS8;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE	OUTER MEMBRANE PROTEIN GNA992.
GN	GNA992.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX	NCBI_TaxID=487;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=A22;
RX	MEDLINE=20175756; PubMed=10710308;
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA	Moxon E.R., Grandi G., Rappuoli R.;
RT	"Identification of Vaccine Candidates Against Serogroup B
RL	Meningococcus by Whole-Genome Sequencing.";
DR	EMBL; AF226364; AAF42513.1; -.
SQ	SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;
Query Match	27.3%; Score 162; DB 2; Length 598;
Best Local Similarity	100.0%; Pred. No. 3e-147;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Best Local Similarity 100.0%; Pred. No. 3e-147;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 306 GEGLVTAKEVIDAVNKAGWRMKTGTANGQTGOADKFEETVTSCTNVTTFASGKGTATVSKD 365
|||||
Db 311 GEGLVTAKEVIDAVNKAGWRMKTGTANGQTGOADKFEETVTSCTNVTTFASGKGTATVSKD 370
|||||
QY 366 DQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVLISGNVSPSKGMDETVNIIN 425
|||||
Db 371 DQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVLISGNVSPSKGMDETVNIIN 430
|||||
QY 426 AGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPTLSVD 467
|||||
Db 431 AGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPTLSVD 472
|||||
```

RESULT 8

```
Q9JPS7 ID Q9JPS7 PRELIMINARY; PRT; 591 AA.
AC Q9JPS7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992..
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;
```

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.7e-146;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 306 GEGLVTAKEVIDAVNKAGWRMKTGTANGQTGOADKFEETVTSCTNVTTFASGKGTATVSKD 365
|||||
Db 304 GEGLVTAKEVIDAVNKAGWRMKTGTANGQTGOADKFEETVTSCTNVTTFASGKGTATVSKD 363
|||||
QY 366 DQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVLISGNVSPSKGMDETVNIIN 425
|||||
Db 364 DQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVLISGNVSPSKGMDETVNIIN 423
|||||
QY 426 AGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPTLSVD 466
|||||
Db 424 AGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPTLSVD 464
|||||
```

RESULT 9

```
Q93QY3 ID Q93QY3 PRELIMINARY; PRT; 591 AA.
AC Q93QY3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
OS NHHA.
OC Neisseria meningitidis.
```

```
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157606; AAK68867.1; -.
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;
```

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.7e-146;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 306 GEGLVTAKEVIDAVNKAGWRMKTGTANGQTGOADKFEETVTSCTNVTTFASGKGTATVSKD 365
|||||
Db 304 GEGLVTAKEVIDAVNKAGWRMKTGTANGQTGOADKFEETVTSCTNVTTFASGKGTATVSKD 363
|||||
QY 366 DQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVLISGNVSPSKGMDETVNIIN 425
|||||
Db 364 DQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVLISGNVSPSKGMDETVNIIN 423
|||||
QY 426 AGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPTLSVD 466
|||||
Db 424 AGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPTLSVD 464
|||||
```

RESULT 10

```
Q9JRI8 ID Q9JRI8 PRELIMINARY; PRT; 591 AA.
AC Q9JRI8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
DE PROTEIN).
GN GNA992 OR NMB0992 OR NHHA.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B; BZ169, BZ83, AND H44/76;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzia M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
```

RL Science 287:1809-1815(2000).

```

[3]
RN SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelmann M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -
DR EMBL; AE002450; AAF41395.1; -
DR EMBL; AF226367; AAF42516.1; -
DR EMBL; AF226370; AAF42519.1; -
DR EMBL; AF226374; AAF42523.1; -
DR EMBL; AF157611; AAK68872.1; -
DR TIGR; NMB0992; -
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 27.1%; Score 161; DB 16; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTVSGTNVTFASGKTTATVSKD 365
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTVSGTNVTFASGKTTATVSKD 363
Qy 366 DQGNITVMYDVGDNALVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNIN 425
Db 364 DQGNITVMYDVGDNALVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNIN 423
Qy 426 AGNNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLTSLVD 466
Db 424 AGNNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLTSLVD 464

RESULT 11
Q9AQF0 ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC38;
RA Peak I.R., Srikantha Y., Dieckelmann M., Moxon E.R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 27.1%; Score 161; DB 2; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTVSGTNVTFASGKTTATVSKD 365
Db 305 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFEVTVSGTNVTFASGKTTATVSKD 364
Qy 366 DQGNITVMYDVGDNALVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNIN 425
Db 365 DQGNITVMYDVGDNALVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNIN 424
Qy 426 AGNNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLTSLVD 466
Db 425 AGNNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLTSLVD 465
```

```

RESULT 12
Q9JPI0 ID Q9JPI0 PRELIMINARY; PRT; 589 AA.
AC Q9JPI0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGP165, 90/18311, AND 93/4286;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Conanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
  Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226384; AAF42533.1; -
DR EMBL; AF226362; AAF42511.1; -
DR EMBL; AF226363; AAF42512.1; -
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95D4868566A6 CRC64;

Query Match 23.2%; Score 138; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 YDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIET 433
Db 369 YDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIET 428
Qy 434 RGNKNIDIAATSMTPQFSSVSLGAGADAPTLTSLVDDEGALNVGSKDANKPVRTNVPAGVKE 493
Db 429 RGNKNIDIAATSMTPQFSSVSLGAGADAPTLTSLVDDEGALNVGSKDANKPVRTNVPAGVKE 488
Qy 494 GDVTNVAQLKGVAQNINN 511
Db 489 GDVTNVAQLKGVAQNINN 506

RESULT 13
Q93QY1 ID Q93QY1 PRELIMINARY; PRT; 589 AA.
AC Q93QY1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=p20;
RA Peak I.R., Srikantha Y., Dieckelmann M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157610; AAK68871.1; -
SQ SEQUENCE 589 AA; 61448 MW; 1F1A80CD610CB230 CRC64;
```

```
Query Match      23.2%; Score 138; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
DB 369 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 428
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493
DB 429 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 488
QY 494 GDVTNVAQLKGVAQNLNN 511
DB 489 GDVTNVAQLKGVAQNLNN 506

RESULT 14
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RC STRAIN=NGE28;
RA MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Scorni E., Zuo P.,
RA Brooker M., Ruidt E., Knapp B., Blair E., Mason I., Fettel H.,
RA Hood B.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.K., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match      23.2%; Score 138; DB 2; Length 590;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
DB 370 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 429
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493
DB 430 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 489
QY 494 GDVTNVAQLKGVAQNLNN 511
DB 490 GDVTNVAQLKGVAQNLNN 507

RESULT 15
ID Q93QY2 PRELIMINARY; PRT; 592 AA.
AC Q93QY2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
```

```
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RC STRAIN=H41;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157609; AAK68870.1; -.
SQ SEQUENCE 592 AA; 61869 MW; F9403A0B4A18EEA7 CRC64;

Query Match      23.2%; Score 138; DB 2; Length 592;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
DB 372 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493
DB 432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 491
QY 494 GDVTNVAQLKGVAQNLNN 511
DB 492 GDVTNVAQLKGVAQNLNN 509

Search completed: September 5, 2002, 10:39:11
Job time: 428 sec
```



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:31:59 ; Search time 58.77 Seconds  
(without alignments)  
1116.975 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHFGASASVGQW 591

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 15

Total number of hits satisfying chosen parameters: 48

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_032802.\*

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	97.0	591	20	AA27202
2	573	97.0	591	20	AA23746
3	573	97.0	591	22	AAU06171
4	525	88.8	591	20	AA23741
5	525	88.8	591	22	AAU06175
6	458	77.5	512	22	AAU06182
7	432	73.1	592	20	AA23737
8	381	64.5	433	22	AAU06185
9	367	62.1	591	21	AAU57045
10	355	60.1	407	22	AAU06184
11	355	60.1	502	22	AAU06186

12	175	29.6	245	20	AA27201	Amino acid sequenc
13	161	27.2	594	20	AA23740	A surface protein
14	161	27.2	594	21	AA57044	BAS029 amino acid
15	161	27.2	594	22	AAU06174	N. meningitidis BG
16	137	23.2	592	20	AA27203	Amino acid sequenc
17	137	23.2	592	22	AAU06180	N. meningitidis Z2
18	117	19.8	594	20	AA23739	A surface protein
19	117	19.8	594	22	AAU06179	N. meningitidis B2
20	117	19.8	598	20	AA23742	A surface protein
21	117	19.8	598	22	AAU06177	N. meningitidis H1
22	116	19.6	116	21	AA37832	Neisserial conserv
23	116	19.6	599	20	AA23743	A surface protein
24	116	19.6	599	22	AAU06176	N. meningitidis H3
25	103	17.4	513	22	AAU06183	N. meningitidis H4
26	103	17.4	592	20	AA23744	A surface protein
27	103	17.4	592	22	AAU06172	N. meningitidis H4
28	93	15.7	589	20	AA23745	A surface protein
29	93	15.7	589	22	AAU06173	N. meningitidis P2
30	93	15.7	598	20	AA23738	A surface protein
31	93	15.7	598	22	AAU06178	N. meningitidis B2
32	72	12.2	72	21	AA37830	Neisserial conserv
33	59	10.0	604	22	AAU06181	N. meningitidis su
34	56	9.5	56	21	AA37827	Neisserial conserv
35	53	9.0	53	21	AA37828	Neisserial conserv
36	23	3.9	23	21	AA37824	Neisserial conserv
37	20	3.4	20	21	AA37831	Neisserial conserv
38	19	3.2	19	21	AA51546	YadA homologous pe
39	19	3.2	19	21	AA51547	YadA homologous pe
40	19	3.2	1098	17	AA99392	Haemophilus adhesi
41	18	3.0	2353	17	AA99393	Haemophilus adhesi
42	18	3.0	2411	21	AA23860	Haemophilus Influe
43	17	2.9	17	21	AA37818	Neisserial conserv
44	17	2.9	1094	21	AA323858	Haemophilus Influe
45	16	2.7	16	21	AA37819	Neisserial conserv
46	16	2.7	16	21	AA37829	Neisserial conserv
47	15	2.5	15	21	AA37822	Neisserial conserv
48	15	2.5	15	21	AA37825	Neisserial conserv

#### ALIGNMENTS

RESULT 1  
AA27202  
ID AA27202 standard; Protein; 591 AA.  
XX AA27202;  
AC AA27202;  
DT 24-SEP-1999 (first entry)  
XX Amino acid sequence of N. meningitidis protein ORF40-1.  
DE Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
XX bacterial infection; treatment.  
OS Neisseria meningitidis.  
XX WO936544-A2.  
XX 22-JUL-1999.  
PD 14-JAN-1999; 99WO-IB00103.  
XX 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-00019015.  
XX (CHIR-) CHIRON SPA.  
PA Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
PI WPI; 1999-444400/37.  
XX N-PSDB; AAX99124.  
DR

XX New protein and its nucleotide sequence, useful in vaccines or  
 PT diagnostic compositions for treating and/or preventing *Neisseria*  
 PT meningitidis infections  
 XX  
 PS  
 PS Claim 1; Page 62; 123pp; English.  
 XX  
 CC The invention provides proteins (AAY27201-245) from *Neisseria*  
 CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
 CC encoding the proteins. Compositions comprising the protein, nucleic acid  
 CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
 CC vaccine composition or a diagnostic composition. The composition is also  
 CC useful for treating or preventing an infection due to *Neisseria*  
 CC bacteria, especially *Neisseria meningitidis*.  
 XX  
 XX Sequence 591 AA;

Query Match 97.0%; Score 573; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 VSELRNHTKRASATVKTAVLATLLFATVOASANNEEQEEDLYLDPVQRTVAVILVNSDK 78  
 Db 19 vseltrnhtkrasatvktavlatllfatvgasanneeqeedlyldpvqrtvavilvnsdk 78  
 QY 79 EGTGEKEKVEENSWAVYFNEKGYLTAREITLKAGDNLIKONGTNTFYSLKKDLTDLTS 138  
 Db 79 egtgekekeveensdwwavyfnekgvltareitlkagdnlikongntfnfyslkkdltlts 138  
 QY 139 VGTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDLLNTGATTN 198  
 Db 139 vgteklsfsangknvnitsdtkglnfaketagntgdtvhlngigstltdllntgattn 198  
 QY 199 VTNDNVTDDEKKRAASVKDVLNAGWNITKGVKPGCTTASDNVDFVRYDTVEFLSADTKTTT 258  
 Db 199 vtndnvtddkkraasvkdvlmagwnitkgvpgcttasdnvdfvrydtveflsadtkttt 258  
 QY 259 VNVESKDNKGKTEVKGAKTSVKEKDGKLVGCKDGENGSSDTDEGCLVTAKEVIDAVN 318  
 Db 259 vnvesskdnkgktevkgaktsvkekdgklvgckdgenngssdtdegeclvtakevidavn 318  
 QY 319 KAGWRMKTITANGQTQADKFEVVTSGTNVTFASGKGTATVSKDDGNTVWYDVNVGD 378  
 Db 319 kagwrmtktitangqtqadkfevtsgtnvtfasgkgtatvskddgntvmydvnvgd 378  
 QY 379 ALNVNQLNSGWNLDKSAVAGSSGKVTISGNVSPSKGKMDETVNIAGNNEITRNGKNID 438  
 Db 379 alnvnglqnsqwnldskavagssgkvtisgnvpsksgkmdetvniagnnieitrngknid 438  
 QY 439 IATSMTPQFSSVSLGAGADAPTLSVDGDLNVGSKKDNKRPVRIITNAPGVKEGDTVNVAG 498  
 Db 439 iatmtptpfssvslgagadaptlsvdgdalnvgskkdnkprvritnvapgvkegdvtnvag 498  
 QY 499 LKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPCKSMMAITGGTYRGEAGYAIGY 558  
 Db 499 lkgvaqnlnrnidnvgnaraglaqaiataglvqaylpcksmmaiggtyrgeagyaigy 558  
 QY 559 SSISDGGNWIKTGASNSRGHFGASASVGYOW 591  
 Db 559 ssisdggnwiiktgasnsrghfgasasvgyow 591

RESULT 2  
 AAY23746  
 ID AAY23746 standard; Protein; 591 AA.  
 XX  
 AC AAY23746;  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 XX A surface protein of *Neisseria meningitidis*.  
 DE  
 XX

KW Surface protein; surface glycoprotein; infection; vaccine;  
 KW immunoreactive peptide.  
 XX  
 OS *Neisseria meningitidis*.  
 XX  
 PN WO9931132-A1.  
 XX  
 XX 24-JUN-1999.  
 XX  
 XX 14-DEC-1998; 98WO-AU01031.  
 XX  
 XX 12-DEC-1997; 97GB-0026398.  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 PA (UYQU) UNIV QUEENSLAND.  
 XX  
 XX Jennings MP, Moxon ER, Peak IRA;  
 PI  
 XX  
 XX WPI; 1999-418754/35.  
 DR N-PSDB; AAX85798.  
 DR  
 XX *Neisseria meningitidis* surface proteins useful for treating *N.*  
 PT meningitidis infections  
 XX  
 XX Claim 1; Page 127-128; 132pp; English.  
 PS  
 XX  
 CC The present sequence represents a surface protein of *Neisseria*  
 CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection of diagnosis of *N. meningitidis* infection in humans.  
 CC The *N. meningitidis* surface glycoproteins can also be used to  
 CC prevent or treat *N. meningitidis* infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 XX  
 XX Sequence 591 AA;

Query Match 97.0%; Score 573; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 VSELRNHTKRASATVKTAVLATLLFATVOASANNEEQEEDLYLDPVQRTVAVILVNSDK 78  
 Db 19 vseltrnhtkrasatvktavlatllfatvgasanneeqeedlyldpvqrtvavilvnsdk 78  
 QY 79 EGTGEKEKVEENSWAVYFNEKGYLTAREITLKAGDNLIKONGTNTFYSLKKDLTDLTS 138  
 Db 79 egtgekekeveensdwwavyfnekgvltareitlkagdnlikongntfnfyslkkdltlts 138  
 QY 139 VGTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDLLNTGATTN 198  
 Db 139 vgteklsfsangknvnitsdtkglnfaketagntgdtvhlngigstltdllntgattn 198  
 QY 199 VTNDNVTDDEKKRAASVKDVLNAGWNITKGVKPGCTTASDNVDFVRYDTVEFLSADTKTTT 258  
 Db 199 vtndnvtddkkraasvkdvlmagwnitkgvpgcttasdnvdfvrydtveflsadtkttt 258  
 QY 259 VNVESKDNKGKTEVKGAKTSVKEKDGKLVGCKDGENGSSDTDEGCLVTAKEVIDAVN 318  
 Db 259 vnvesskdnkgktevkgaktsvkekdgklvgckdgenngssdtdegeclvtakevidavn 318  
 QY 319 KAGWRMKTITANGQTQADKFEVVTSGTNVTFASGKGTATVSKDDGNTVWYDVNVGD 378  
 Db 319 kagwrmtktitangqtqadkfevtsgtnvtfasgkgtatvskddgntvmydvnvgd 378  
 QY 379 ALNVNQLNSGWNLDKSAVAGSSGKVTISGNVSPSKGKMDETVNIAGNNEITRNGKNID 438  
 Db 379 alnvnglqnsqwnldskavagssgkvtisgnvpsksgkmdetvniagnnieitrngknid 438  
 QY 439 IATSMTPQFSSVSLGAGADAPTLSVDGDLNVGSKKDNKRPVRIITNAPGVKEGDTVNVAG 498  
 Db 439 iatmtptpfssvslgagadaptlsvdgdalnvgskkdnkprvritnvapgvkegdvtnvag 498



Db 439 tatsmtpfssvslgagadapltlsvdgdalnvgskkdkpvriltvnapgvkegdvtnvaq 498  
QY 499 LKGVAQNLRNDRVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIQY 558  
Db 499 lkgvaqnlmnrldnvdgnaragiataglvqaylpgksmma199gtyrgeagyaigy 558  
QY 559 SSISDGGNWIKGTASGNSRHFSGASVGYQW 591  
Db 559 ssisdggnwilkgtasgnsrghfgasasvgyqw 591  
RESULT 3  
AAU06171  
ID AAU06171 standard; Protein: 591 AA.  
XX  
AC AAU06171;  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.  
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.  
XX Neisseria meningitidis strain PMC21.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..51  
FT Region /label= Signal\_peptide  
FT Region 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..108  
FT /label= V1  
FT /note= "Variable region 1"  
FT 52..591  
FT /label= Mature\_NhhA  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12"  
FT 109..120  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 121..124  
FT /label= V2  
FT /note= "Variable region 2"  
FT 125..188  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 189..210  
FT /label= V3  
FT /note= "Variable region 3"  
FT 211..229  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 230..236  
FT /label= V4  
FT /note= "Variable region 4"  
FT 237..591  
FT /label= C5  
FT /note= "Conserved region 5"  
XX  
PN WO200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI; 2001-488774/53.

DR N-PSDB; AAS09161.  
XX New NhhA surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX Claim 9; Fig 1; 9lpp: English.  
PS  
PS  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen NhhA  
CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen NhhA  
CC from N. meningitidis strain PMC21 is 1 of 10 NhhA polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX Sequence 591 AA;  
SQ  
Query Match 97.0%; Score 573; DB 22; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDLYLDPVQRTVAVLIVNSDK 78  
Db 19 vseltrnhtkrasatvktavlatllfatvqasanneeqedlylqpqrtvavlivnsdk 78  
QY 79 EGTGEKEKVEENSDWAVTFNEKGVLTAREITLKAGDNLIKONGNFYSLKKDLTSLTS 138  
Db 79 egtgekekeveensdwavtfnekgvltareitlkagdnlikongnftyslkkdltdits 138  
QY 139 VGTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDITVHLNGIGSTLDTLLNGATTN 198  
Db 139 vgteklisfsangknvnitsdtkglnfaketagntgdtvhlnglgsstltdtllngattn 198  
QY 199 VTNDNVTDDEKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDYVEFLSADTKTTT 258  
Db 199 vtndnvtddekkraasvkdvlmagwnikgvkpgttasdnvdfvrydytveflsadtkttt 258  
QY 259 NVVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGENGSSTDEGGLVTAKEVIDAVN 318  
Db 259 nvveskdngkktevkigaktsvikekdgklvtgdkgengsstdeglvtakevidavn 318  
QY 319 KAGWRMKTTTANGOTGOADKPFETVTSNTVTFASGKGTATATVSKDDOGNITVMYDVNVGD 378  
Db 319 kagwrmktttangotgcgqadkpfetvtsntvtfasgkgtattatvskddqgnitvmydvnvgd 378  
QY 379 ALNVNQLONGSNWNLDSKAVAGSSGKVISGNVSPSKGKMDETVYNINAGNNIETRNGKNID 438  
Db 379 alnvnglqnsngwnldskavagssgkvisgnvspskgmdetvyninagnnieitrngknid 438  
QY 439 IATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDNKPVRIITWVAPGVKCDVTVNAQ 498  
Db 439 iatsmtpfssvslgagadaptlsvdgdalnvgskkdkpvriltvnapgvkegdvtnvaq 498  
QY 499 LKGVAQNLRNDRVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIQY 558  
Db 499 lkgvaqnlmnrldnvdgnaragiataglvqaylpgksmma199gtyrgeagyaigy 558  
QY 559 SSISDGGNWIKGTASGNSRHFSGASVGYQW 591  
Db 559 ssisdggnwilkgtasgnsrghfgasasvgyqw 591  
RESULT 4  
RAY23741



PT New NhA surface antigen polypeptides and polynucleotides from  
PT *Neisseria meningitidis*, useful in producing vaccines for treating or  
PT preventing broad spectrum of *Neisseria meningitidis* -  
XX  
XX  
XX Claim 9; Fig 1; 91pp; English.  
CC  
CC The present invention relates to the isolation of novel *Neisseria*  
CC *meningitidis* mutant polypeptides of the surface antigen NhA  
CC (AAU06182-AAU06186). The modified or mutant NhA polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC in the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of *N. meningitidis*, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of *N. meningitidis* strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen NhA  
CC from *N. meningitidis* strain EG329 is 1 of 10 NhA polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
XX the present invention.  
XX Sequence 591 AA;  
SQ

```
Query Match      88.8%; Score 525; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

67	QY	RTVAVLIVNSDKSGTGEKEKVEENSOWAVYFNEKGVLTAIREITLKAGDNLKIKQNGTNP	126
67	Db	rtvavlivnsdksgtgekekeveensdwayvfynekvgltareitlkagdnlikqngntf	126
127	QY	YSLKKDLTDLTSVGTPEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTL	186
127	Db	yslkkdltdltsvgtpeklfsangknvntsdtkglnfaketagngdtvhlngigstl	186
187	QY	TDTLNLTGATNTVNDNVTDDEKkraasvkdvlNAGWNlKGvKPGTfASDNVDFVRYTDT	246
187	Db	tdtllntgatntvndnvtddekkrasvkdvlNagwnlkgvKpgtFasdnvdfvrytdt	246
247	QY	VEFLSADTKTTTVNESKONGKRTYKlGAKTSVlKEKDGKLVTKDKGEGSSSTDEGBG	306
247	Db	veflsadtktttvneskdngkktvklgaktsvlkekdgklvtgdkdGEGSSSTdegeg	306
307	QY	LVTAKFVIDAVNAGWRMKTtTANGOTGQADKFETVTSCTNTVTFASGKTTTATVSKDDOG	366
307	Db	lvtakevidavnagwrMktTtAngotgqadkfetvtsgtnvtfAsgkttatvskddg	366
367	QY	NITVMYDENVGDALNVNOLNSGWNlDSKAVAGSSGKVlSGNVSPSGKGMDETVINAGN	426
367	Db	nltvmYdenvgdalnvnqlnsgwnlDSKavagssgkvlsGnvspsgkGmdetvinagn	426
427	QY	NIEITRNGKNIDlATSMTPOFSSVSLGAGADPTLlSVDGDALNVSGKDNKPNVITINAP	486
427	Db	nieitrngknidiatSmtPofssvslgagadptlSvdgdalnvsgkdnkPvritnVap	486
487	QY	GVKEGDTVNTVAQLKGVAQNlNNRlDlNVdGNARAGlTAAQlATAGLVQAYlPGKSMAlGGG	546
487	Db	gvkegdtvntvaqlkgvaqnlnnrIdnvDgnaragIaqaIataglvqaylpgkSmaIggg	546
547	QY	TYRGEAGYAlGYSISIDGGWNlIKGTASGNSRHFQASASVGYQW	591
547	Db	tyrgeagyaIgySisdggwnlIkgtasgnsrhFqasasvgyqW	591

RESULT	6
AAU06182	
ID	AAU06182 standard; Protein; 512 AA.
XX	
XX	
AC	AAU06182;
XX	
XX	
DT	24-OCT-2001 (first entry)
XX	

DE	N. meningitidis PMC21 Nhha deletion mutant #1.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW	mutant; mutein.
XX	
OS	Neisseria meningitidis strain PMC21.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	Peptide
FT	1..51
FT	/label= Signal_peptide
FT	Protein
FT	52..512
FT	/label= Mature_Nhha_deletion_mutant_#1
FT	/note= "Predicted mature protein, specifically
FT	claimed in claim 12"
XX	
PN	WO200155182-A1.
XX	
PD	02-AUG-2001.
XX	
XX	25-JAN-2001; 2001WO-AU000069.
XX	
XX	25-JAN-2000; 2000US-0177917.
PR	
XX	(UYQU ) UNIV QUEENSLAND.
PA	
XX	
PI	Peak IRA, Jennings MP;
XX	
DR	WPI; 2001-488774/53.
DR	N-PSDB; AAS09172.
XX	
PT	New Nhha surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
XX	Claim 12; Fig 5; 9lpp; English.
PS	
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhha
CC	(AAU06183-AAU06186). The modified or mutant Nhha polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnosis, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	would be expected from a corresponding wild-type surface antigen.
CC	The present sequence represents N. meningitidis strain PMC21 surface
CC	antigen Nhha deletion mutant #1.
XX	
SQ	Sequence 512 AA;

```
Query Match          77.5%; Score 458; DB 22; Length 512;
Best Local Similarity 100.0%; Pred. NO. 0;
```

Qy	134	TDTSVGTGTEKLSFSANGKNVNI	SDTKGLNFAKETAGTNGD	TTVHLUNGIGSTLTDLLNT	193	
Db	55	tdttsvgtelsfsangknvni	sdtkglnfaketagntd	ttvhlungigstltdllnt	114	
Qy	194	GATTNTNDNVTDDEKKRAASV	KDYLNAGNNIKGVKPG	TTASDNVDFVRYDVFELSAD	253	
Db	115	gattntndnvtddekkraasv	kdylnagwnikgvpgt	casdnvdfvrydytvefisd	174	
Qy	254	TKTTTVNESKDNGKTEVKIG	AKTSVIKESDKGLTGD	KGNGSGSTDEGEGLTAKEV	313	
Db	175	tktttvneskdngkktevkig	aktsvikekdglvtg	kdgngsgstdegegltakev	234	
Qy	314	IDAVNKAGWRMKTTTANG	QTQGDQADKPFETV	SGTNVTFASGKGT	TTAVSKDDQGNITVMXD	373
Db	235	idavnkagwrmktttango	qtgdqadkfetvsgtnv	faskgtatvskddqgnitv	myd	294

QY 374 VNVGDALNVNOLNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIETRN 433  
Db 295 vnvgdalnvnlqnswnldskavagssgkvisgnvspskgkmdetvnnagnnietrn 354  
QY 434 GKNIDIASMTFQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPKVRITNVAPGVKEGDV 493  
Db 355 gknidiasmtpqfssvslgagadaptlsvdgdalnvsgkdknkpvrtnvapgvkegdv 414  
QY 494 TNVAOLKGVNOLNRRIDNVGNARAGIAQAIATAGLVQAYLPKSMMAIGGGTYRGEAG 553  
Db 415 tnvaqlkgvaqlnrridnvdgnaragiaqaiataglvqaylpqksmmaigggtyrgeag 474  
QY 554 YAIYSSISDGNWIIKGTASGNSRHFAGASASVGYQW 591  
Db 475 yaigyssisdggnwiikgtasgnrghfgasasvgyqw 512

## RESULT 7

AAU06185  
ID AAY23737 standard; Protein; 592 AA.

AC AAY23737;

XX 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX Neisseria meningitidis.

OS WO9931132-A1.

PN 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS) ISIS INNOVATION LTD.

PA (UYOU ) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.

DR N-PSDB; AAX85788.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 86-87; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 592 AA;

Query Match 73.1%; Score 432; DB 20; Length 592;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 DLYLDPVORTVAVILVNSDEGTEGKEKEVEENSDWAVYFNEKGYLTAREITLKGADNLKI 118  
Db 60 dlyldpvtvavilvnsdtegtcgekeveensdwavinekyvltareitlkgadnlki 119

QY 119 KONGTNTYYSKKDLTDLTTSVTEKLSFSSANGKNVNITSDTKGLNFAKETAGTNGDTTVH 178  
Db 120 kngtnfnfyskkdldtldtsvgteklsfsangknvnitstdtkglnfaketagtngdttvh 179  
QY 179 LKNGISTLTDLTLLNTGATTNTVNDNVTDDPKRAASVKDVLNAGWNKIGVKPPTASDNV 238  
Db 180 lngigstltdltnlgattntvndnvtddkakraasvkdvlnagwnlkgvkkpgttasdnv 239  
QY 239 DFRVRYDVEEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKDKKGENG 298  
Db 240 dfrvrydveeflsadtktttvnnveskdngkktevkigvktsvikekdgklvtgdkdeng 299  
QY 299 SSTDEGEGLVTAKEVIDAVNKAQRMTTNTTANGOTQADKPTETVTSNGNVTFASGKGTGA 358  
Db 300 sstdegeglvtakevidavnkagrmkttntangotqgqdkfetvtsngntvtfasgkgtta 359  
QY 359 TVSKDDOGNITVMYDVNVGDALNVNOLNSGNLDSKAVAGSSGKVISGNVSPSKGKMD 418  
Db 360 tvskddognitvmvdyvngdnlvnlqnswnldskavagssgkvisgnvspskgkmd 419  
QY 419 TVNINAGNNIETRNKKNIDIASMTFQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPK 478  
Db 420 tvninagnnieltrngknidiasmtpqfssvslgagadaptlsvdgdalnvsgkdknkp 479  
QY 479 VRITNVAPGVKEGDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIATAGLVQAYLPKG 538  
Db 480 vritnvapgvkegdvtnvaqlkgvaqlnrridnvdgnaragiaqaiataglvqaylpkg 539  
QY 539 SMMAIGGGTYRGEAGYAIYSSISDGNWIIKGTASGNSRHFAGASASVGYQW 591  
Db 540 smmaigggtyrgeagyaigyssisdggnwiikgtasgnrghfgasasvgyqw 592

## RESULT 8

AAU06185  
ID AAU06185 standard; Protein; 433 AA.

AC AAU06185;

DT 24-OCT-2001 (first entry)

DE N. meningitidis PMC21 Nhha deletion mutant #3.

KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; mutein.

OS Neisseria meningitidis strain PMC21.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..51

FT Protein 52..433

FT /label= Mature\_Nhha\_deletion\_mutant\_#3

FT /note= "Predicted mature protein, specifically

claimed in claim 12"

PN WO200155182-A1.

PD 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYOU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

XX WPI: 2001-488774/53.

DR N-PSDB; AAS09175.

PT	New NhA surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 12; Fig 8; 9lpp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen NhA
CC	(AAU06182-AAU06186). The modified or mutant NhA polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	would be expected from a corresponding wild-type surface antigen.
CC	The present sequence represents N. meningitidis strain PMC21 surface
CC	antigen NhA deletion mutant #3.
XX	
XX	Sequence 433 AA;
SQ	
Query Match 64.5%; Score 381; DB 22; Length 433;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	211 RAASVKDVLNAGWNIKGVPKPTTASDNVDFRYDTVEFLSADTKTTTVNVESKDNGKKT 270
Db	
QY	53 raasvkdvl Nagwnikgvpkpttasdnvdfrydtveflsadtktttvnveskdngkkt 112
Db	
QY	271 EVKIGAKTSVIKEKDGLKVLTGCKDGSGSTDEGEGLVTAKEVIDAVNKAGRMRMTTTAN 330
Db	
QY	113 evkigaktsvikekdgklvtgckdgsgstdegeglvtakevidavnkagwrmktttan 172
Db	
QY	331 GOTGGADKFEEVTSGTNVTFASGKGTATYVSKDDQGNITPVWDVNVDALNVNQIQLNSGW 390
Db	
QY	173 gdtgdqdkfetvtsgrntvfaskgttatsvkddqgnitvm ydvnvgdalnvqlqnsqw 232
QY	391 NLDSKAVAGSSGKVTSGNVSPSKGMDETVININAGNNIETRNGKNIDIA TSMT PQFSSV 450
Db	
QY	233 nl dskavagsgkv lsgnvsp skmdetvininagnnietrngknidiat smtpqfssv 292
QY	451 SLGAGADAPTL SVGDG DALNVGSKDKDPVRITNVAFPVKEGDV TNVAQLKGVAQNLNRRI 510
Db	
QY	293 slgagadaptlsvgdgalnvgs kdkdpvr itnvapvk egdvt nvaqlkgvaqlnrri 352
QY	511 DNVVDGNARAGINAQTATAGIVQAYLPKSMWATGGTYRGEAGYA IGYSSISDGGNWIIK 570
Db	
QY	353 dnvdvgnaragaiaataglvqaylpdksmma igggtyrge agyaigyssi sdgggnwiik 412
QY	571 GTASGNSRGHFGASASVG YQW 591
Db	
QY	413 gtasgnsrg hfgasasy qyw 433
RESULT	9
AAV57045	
ID	AAV57045 standard; Protein; 591 AA.
XX	
AC	AAV57045;
XX	
DT	XX
DT	XX
DT	21-FEB-2000 (first entry)
XX	
DE	BASB029 amino acid sequence from N. meningitidis strain H44/76.
KX	
WW	BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnostics;
KW	Infection; treatment; prevent; antibacterial drug.
XX	
OS	Neisseria meningitidis.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 90
FT	/note= "Encoded by AAT"

FT	Misc-difference 92	/note= "Encoded by GAT"
FT	Misc-difference 98	/note= "Encoded by AAC"
FT	Misc-difference 108	/note= "Encoded by AATC"
FT	Misc-difference 123	/note= "Encoded by ACA"
FT	Misc-difference 269	/note= "Encoded by AAA"
FT	Misc-difference 389	/note= "Encoded by CGT"
XX	WO9958683-A2.	
PN	18-NOV-1999.	
PD	07-MAY-1999;	99WO-EP03255.
PF	13-MAY-1998;	98GB-0010276.
XX	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.	
PA	Ruelle J;	
XX	WPI; 2000-053103/04.	
DR	N-PSDB; AAZ39865.	
XX	New polypeptide from neisseria meningitidis useful for diagnosis,	
PT	treatment or prevention of bacterial infections in mammal	
XX	Claim 4; Fig 2; 74pp; English.	
XX	This is the Nisseria meningitidis BASB029 amino acid sequence from	
CC	serogroup B strain H44/76. The BASB029 protein is homologous to the	
CC	Haemophilus influenzae surface fibril (HSF) protein. The invention	
CC	relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and	
CC	polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.	
CC	BASB029 polypeptides are useful in a method of diagnosing a Neisseria	
CC	meningitidis infection in a mammal. Compositions containing BASB029	
CC	polynucleotides and polypeptides are useful for generating an immune	
CC	response in an animal. A therapeutic composition comprising an antibody	
CC	directed against BASB029 is useful in treating humans with Neisseria	
CC	meningitidis disease. The polynucleotide is useful in the diagnosis of	
CC	the stage of infection, type of infection, susceptibility to an	
CC	infection which results from increased or decreased expression of the	
CC	polynucleotide, and for therapeutic or prophylactic purposes,	
CC	particularly genetic immunisation. Antibodies against BASB029	
CC	polynucleotides and polypeptides are also useful for treating infections	
CC	particularly bacterial infections. The protein is useful in the	
CC	screening and development of antibacterial drugs. Fused recombinant	
CC	protein is useful for the stimulation of the immune system of an organism	
CC	receiving the protein.	
XX		
SQ	Sequence	591 AA;
Query Match            62.1%; Score 367; DB 21; Length 591;		
Best Local Similarity   99.8%; Pred. No. 0;		
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	124	NFTYSLLKKDLTLTSVGTEKLFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLHGIG 183 
Db	124	nftysllkddlclslsvgteklsfsangnkvnltstdkglnfakecagntgdttvhlhgig 183 
QY	184	STLTDTLNTGATTNVTTNDNYTDDDEKKRAASVKDVLNAGWNITKGVPKPGTASDNVDVRT 243 
Db	184	stltdtlntgattnvntndnytddekkraasvkdvlnagwnikgvkpgtasdnvdvrt 243 
QY	244	YDTVEFLISADTKTTTTNNVESKDNGKKTEVKGAKTSVTIKEKDGKLVITGKDKGENSGSTDE 303 
Db	244	ydtveflisadtktttynnveskdngkrtevkgaktsvikekgdgklvitgkdkgensgstde 303 

QY 304 GEGIVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVSKD 363  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 304 GEGIVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVSKD 363  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 364 DQGNITVMTVDVNGDALNVQNSGNWLDKRAVAGSSGKVIISGNVSPSKGMDERVNIN 423  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 364 DQGNITVMTVDVNGDALNVQNSGNWLDKRAVAGSSGKVIISGNVSPSKGMDERVNIN 423  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 424 AGNIEITRNGKNIDIAITMTQPFSSVSLGAGADAPTLSVDGDALNVGSKDKNPKVRIIN 483  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 424 AGNIEITRNGKNIDIAITMTQPFSSVSLGAGADAPTLSVDGDALNVGSKDKNPKVRIIN 483  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 484 VAPGVKEGDTNVAQLKGVQNLNRRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAI 543  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 484 VAPGVKEGDTNVAQLKGVQNLNRRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAI 543  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 544 GGTGYRGEAGYAGYSSISDGGNWIIRKGTASGNSRHFAGASVGYQW 591  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 544 GGTGYRGEAGYAGYSSISDGGNWIIRKGTASGNSRHFAGASVGYQW 591  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10  
 AAU06184  
 ID AAU06184 standard; Protein; 407 AA.  
 AC AAU06184;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis PMC21 Nhha deletion mutant #2.  
 XX  
 DE Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
 KW mutant; mutein.  
 KW  
 XX  
 OS Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..51  
 FT /label= Signal\_peptide  
 FT Protein 52..407  
 FT /label= Mature\_Nhha\_deletion\_mutant\_#2  
 FT /note= "Predicted mature protein, specifically  
 FT claimed in claim 12"  
 XX  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI; 2001-488774/53.  
 DR N-PSDB; AA509174.  
 DR  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 7; 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhha deletion mutant #2.  
 XX  
 SQ Sequence 407 AA;

Query Match 60.1%; Score 355; DB 22; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 237 NVDFVRYDYTVFELISADTKTTTNNVESKDNKGKTEVKIGAKTSVIEKDGKLVTKDKGE 296  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 53 nvdfvrydytvefilsadtktttvnnveskdngkkttevkigaktsviekdgklvtgdkge 112  
 QY 297 NGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGT 356  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 113 ngsstdegeglvtakevidavnkagwmktttangqtgqadkktetvtsctnvtfagkgt 172  
 QY 357 TATVSKDDOGNITVMYDGVNGDALNVQNSGNWLDKRAVAGSSGKVIISGNVSPSKGKM 416  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 173 tatvskddognitvmydgvnvgdalnvqlqnsqwnldskavagssgkvisgnvpskqkm 232  
 QY 417 DETVINAGNIEITRNGKNIDIAITMTQPFSSVSLGAGADAPTLSVDGDALNVGSKKDN 476  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 233 detvinagnnieitrngknidiatmtqpfssvslgagadapltlsvdgdalnvsgkkn 292  
 QY 477 KPVRIITNVAPEVKEGDTNVAQLKGVQNLNRRIDNVGNARAGIAQAIAITAGLVQAYLP 536  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 293 kpvritnvapvkegdtvnaqlkqvqnlrridnvgnaragiagaiaataglvqaylp 352  
 QY 537 GKSMMAIGGTGYRGEAGYAGYSSISDGGNWIIRKGTASGNSRHFAGASVGYQW 591  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 353 gksmmaiggtgyrgeagyagysissdgggnwlikgtasgnsrghfagasasvgyqw 407

RESULT 11  
 AAU06186  
 ID AAU06186 standard; Protein; 502 AA.  
 XX  
 AC AAU06186;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis PMC21 Nhha deletion mutant #4.  
 XX  
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
 KW mutant; mutein.  
 KW  
 XX  
 OS Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..49  
 FT /label= Signal\_peptide  
 FT Protein 50..502  
 FT /label= Mature\_Nhha\_deletion\_mutant\_#4  
 FT /note= "Predicted mature protein, specifically  
 FT claimed in claim 12"  
 XX  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;

```
XX WPI; 2001-488774/53.
DR N-PSDB; AAS09176.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 9; 91pp; English.
PS
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #4.
XX
XX Sequence 502 AA;
SQ
Query Match 60.18; Score 355; DB 22; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 237 NVDFVRYTDTVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVKEKDGKLVTKDKKE 296
Db 148 nvdvrtvdtveflsadtktttnvveskdngkktvkvigaktsvkekdglvkgkde 207
Qy 297 NGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKQFETVTSGTNVTFAAGKGT 356
Db 208 ngsstdegeglvtakevidavnkagrmktttangtqtgqadkfetvtsgtntvfaskgt 267
Qy 357 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLDKAVAGSGGKVISGNVSPSKGKM 416
Db 268 tatvskddqgnitvmvdyvngvdalnvnqlnsgwnldskavagsggkvisgnvspsgkkm 327
Qy 417 DETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDN 476
Db 328 detvniagnnieitrngknidiatstmpqfssvslgagadaptlsvdgdalnvgskkdn 387
Qy 477 KPVRTITNVPAGVKEGDTVNVLAQLKGVAQNLRINDVNGNARAGTAQAIAATAGLVQAYLP 536
Db 388 kpvritnvapgvekdvtnvvaqlkgvaqnlrindvngnragiaqaiaataglvqaylp 447
Qy 537 GKSMMAIGGGTYRGAGYAIGYSSISDGGNWLKGTASGNSRGRHFGASASVGYQW 591
Db 448 gksmmaigggtyrgeagyaigyssisdggnwlikgtasgnsrgrhfgasasvgyqw 502
RESULT 12
AAV27201
ID AAV27201 standard; Protein; 245 AA.
XX
XX AAV27201;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX Amino acid sequence of N. meningitidis protein ORF40.
DE
XX
XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
XX Neisseria meningitidis.
OS
XX
XX WO9936544-A2.
PN
XX
XX 22-JUL-1999.
PD
```

```
XX 14-JAN-1999; 99WO-IB00103.
PF
XX
XX 09-OCT-1998; 98GB-0022143.
PR
XX 14-JAN-1998; 98GB-0000760.
PR
XX 01-SEP-1998; 98GB-0019015.
PR
XX (CHIR-) CHIRON SPA.
PA
XX
XX Grandi G, Masiagnani V, Pizza M, Rappuoli R, Scarlato V;
PI WPI; 1999-444400/37.
XX N-PSDB; AAX99123.
DR
XX
XX New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
PT
XX Claim 1; Page 61; 123pp; English.
PS
XX
XX The invention provides proteins (AAV27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAV99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisserial
CC bacteria, especially Neisseria meningitidis.
CC
XX Sequence 245 AA;
SQ
Query Match 29.6%; Score 175; DB 20; Length 245;
Best Local Similarity 100.0%; Pred. No. 7.7e-169;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 111 KAGDNLKIKQNGTFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTGLNFAKETAG 170
Db 71 kagdnlkikngtftyslkkdldtltsvgtseklfsangnkvnitsdtglnfaketag 130
Qy 171 TNGDTHVHLNGISGTLTDLTLTGATTVNDNVTDDEKKRAASVKDVLNAGWNKGVKP 230
Db 131 tngdthvhlngisgtltdlntgattnvndntddekraasvkdvlntagwnkgvkp 190
Qy 231 GTTASDNVDVRYTDTVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVKEKD 285
Db 191 gttasdnvdfvrytdtveflsadtktttnvveskdngkktvkvigaktsvikekd 245
RESULT 13
AAV23740
ID AAV23740 standard; Protein; 594 AA.
XX
XX AAV23740;
AC
XX
XX 08-SEP-1999 (first entry)
DT
XX
XX A surface protein of Neisseria meningitidis.
DE
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
KW
XX
XX Neisseria meningitidis.
OS
XX
XX WO9931132-A1.
PN
XX
XX 24-JUN-1999.
PD
XX
XX 14-DEC-1998; 98WO-AU01031.
PF
XX
XX 12-DEC-1997; 97GB-0026398.
PR
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYQU ) UNIV QUEENSLAND.
PA
```









GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:32:32 ; Search time 25.6 Seconds  
(without alignments)  
563.888 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKRIYIINWSALNAWAVS.....TASGNSRGHFGASAVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 231628 seqs, 2442594 residues  
Word size : 15  
Total number of hits satisfying chosen parameters: 40

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	97.0	591	4	US-09-377-155-21
2	573	97.0	591	4	US-09-669-974-21
3	525	88.8	591	4	US-09-377-155-11
4	525	88.8	591	4	US-09-669-974-11
5	432	73.1	592	4	US-09-377-155-2
6	432	73.1	592	4	US-09-669-974-2
7	161	27.2	594	4	US-09-377-155-9
8	161	27.2	594	4	US-09-669-974-9
9	117	19.8	594	4	US-09-377-155-7
10	117	19.8	594	4	US-09-669-974-7
11	117	19.8	598	4	US-09-377-155-13
12	117	19.8	598	4	US-09-669-974-13
13	116	19.6	599	4	US-09-377-155-15
14	116	19.6	599	4	US-09-669-974-15
15	103	17.4	592	4	US-09-377-155-17
16	103	17.4	592	4	US-09-669-974-17
17	93	15.7	589	4	US-09-377-155-19
18	93	15.7	589	4	US-09-669-974-19
19	93	15.7	598	4	US-09-377-155-5
20	93	15.7	598	4	US-09-669-974-5
21	19	3.2	658	1	US-08-409-995-5
22	19	3.2	658	3	US-08-685-467-5
23	19	3.2	658	4	US-08-913-942-5
24	19	3.2	1098	1	US-08-409-995-2
25	19	3.2	1098	3	US-08-685-467-2
26	19	3.2	1098	4	US-09-377-155-32
27	19	3.2	1098	4	US-08-913-942-2

28 19 3.2 1098 4 US-09-669-974-32 Sequence 32, Appl  
29 19 3.2 1098 4 US-09-268-347-44 Sequence 44, Appl  
30 18 3.0 1912 1 US-08-409-995-4 Sequence 4, Appl  
31 18 3.0 1912 3 US-08-685-467-4 Sequence 4, Appl  
32 18 3.0 2353 4 US-09-377-155-33 Sequence 33, Appl  
33 18 3.0 2353 4 US-08-913-942-4 Sequence 4, Appl  
34 18 3.0 2353 4 US-09-669-974-33 Sequence 33, Appl  
35 18 3.0 2411 4 US-09-268-347-36 Sequence 36, Appl  
36 17 2.9 1094 4 US-09-268-347-32 Sequence 32, Appl  
37 17 2.9 2354 4 US-09-268-347-47 Sequence 47, Appl  
38 15 2.5 607 1 US-08-409-995-6 Sequence 6, Appl  
39 15 2.5 607 3 US-08-685-467-6 Sequence 6, Appl  
40 15 2.5 607 4 US-08-913-942-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377.155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 97.0%; Score 573; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 VSELTNRNHTKRASATVKTAVALATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
Db 19 VSELTNRNHTKRASATVKTAVALATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
Qy 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFYSLKDKLTDLTS 138  
Db 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFYSLKDKLTDLTS 138  
Qy 139 VGTEKLSFSANGKNYIITSDTKGLNFAKETAGTNGDTTVHLNGIGISTLTDLTLLNTGATTN 198  
Db 139 VGTEKLSFSANGKNYIITSDTKGLNFAKETAGTNGDTTVHLNGIGISTLTDLTLLNTGATTN 198  
Qy 199 VTNDNVTDDKKRAASAKVDVLNAGWNIKGVPKGTTFASDNVDVFRVYDVTFEFSADTKTTT 258  
Db 199 VTNDNVTDDKKRAASAKVDVLNAGWNIKGVPKGTTFASDNVDVFRVYDVTFEFSADTKTTT 258  
Qy 259 VNVESKDNKKTEVKIGAKTSVIKEKDKGLVTKDKGNGSSTDEGEGLVTAKEVIDAVN 318  
Db 259 VNVESKDNKKTEVKIGAKTSVIKEKDKGLVTKDKGNGSSTDEGEGLVTAKEVIDAVN 318  
Qy 319 KAGWRMKTTTANGQTQADKFFETVSGTNVTFASGKGTTFATVSKDDQGNITVYDVNVGD 378  
Db 319 KAGWRMKTTTANGQTQADKFFETVSGTNVTFASGKGTTFATVSKDDQGNITVYDVNVGD 378  
Qy 379 ALNVNOLQNSGNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETTRGNKID 438  
Db 379 ALNVNOLQNSGNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETTRGNKID 438

Db 379 ALNVQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTNINAGNNIEITRNGKNID 438  
Qy 439 IATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPKVRITNVAPGKGDVTNVAQ 498  
Db 439 IATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPKVRITNVAPGKGDVTNVAQ 498  
Qy 499 LKGAQNLNRRIDNVGNRAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
Db 499 LKGAQNLNRRIDNVGNRAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
Qy 559 SSISDGGNWIKGTASGNSRGHFGASASVGYQW 591  
Db 559 SSISDGGNWIKGTASGNSRGHFGASASVGYQW 591

RESULT 2  
US-09-669-974-21  
; Sequence 21 Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 97.0%; Score 573; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 19 VSELTNRHTRKASATVKTAVLATLLFATVQASANNRQEDLYLDPVQRTVAVLIVNSDK 78  
Db 19 VSELTNRHTRKASATVKTAVLATLLFATVQASANNRQEDLYLDPVQRTVAVLIVNSDK 78  
Qy 79 EGTGEKEKVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQNGTNTYSLKKDLTDLTS 138  
Db 79 EGTGEKEKVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQNGTNTYSLKKDLTDLTS 138  
Qy 139 VGTEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDITLLNTGATTN 198  
Db 139 VGTEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDITLLNTGATTN 198  
Qy 199 VTNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTT 258  
Db 199 VTNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTT 258  
Qy 259 VNVESKDNGKTEVKIGAKTSVIEKDGKLVTKDGKGENSSSTDEGEGLVTAKEVIDAVN 318  
Db 259 VNVESKDNGKTEVKIGAKTSVIEKDGKLVTKDGKGENSSSTDEGEGLVTAKEVIDAVN 318  
Qy 319 KAGHRMKTITANGOTQOAKDPETVTSNGNVTTFASGKGTTPATVSKDDQGNITVWYDVNVD 378  
Db 319 KAGHRMKTITANGOTQOAKDPETVTSNGNVTTFASGKGTTPATVSKDDQGNITVWYDVNVD 378  
Qy 379 ALNVQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTNINAGNNIEITRNGKNID 438  
Db 379 ALNVQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTNINAGNNIEITRNGKNID 438

Qy 439 IATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPKVRITNVAPGKGDVTNVAQ 498  
Db 439 IATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPKVRITNVAPGKGDVTNVAQ 498  
Qy 499 LKGAQNLNRRIDNVGNRAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
Db 499 LKGAQNLNRRIDNVGNRAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
Qy 559 SSISDGGNWIKGTASGNSRGHFGASASVGYQW 591  
Db 559 SSISDGGNWIKGTASGNSRGHFGASASVGYQW 591

RESULT 3  
US-09-377-155-11  
; Sequence 11 Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 88.8%; Score 525; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 67 RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQNGTNT 126  
Db 67 RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQNGTNT 126  
Qy 127 YSLKKDLTDLTSVGTGTEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDITVHLNGIGSTL 186  
Db 127 YSLKKDLTDLTSVGTGTEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDITVHLNGIGSTL 186  
Qy 187 TDTLLNTGATTNTVNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNVDFVRYTDT 246  
Db 187 TDTLLNTGATTNTVNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNVDFVRYTDT 246  
Qy 247 VEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIEKDGKLVTKDGKGENSSSTDEGEG 306  
Db 247 VEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIEKDGKLVTKDGKGENSSSTDEGEG 306  
Qy 307 LVTAKEVIDAVNKAHRMKTITANGOTQOAKDPETVTSNGNVTTFASGKGTTPATVSKDDQ 366  
Db 307 LVTAKEVIDAVNKAHRMKTITANGOTQOAKDPETVTSNGNVTTFASGKGTTPATVSKDDQ 366  
Qy 367 NIIVWYDVNVDGDLNVQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTNINAGN 426  
Db 367 NIIVWYDVNVDGDLNVQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTNINAGN 426  
Qy 427 NIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPKVRITNVAP 486  
Db 427 NIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPKVRITNVAP 486  
Qy 487 GVKEGDVTNVAQLKGAQNLNRRIDNVGNRAGIAQAIATAGLVQAYLPGKSMMAIGGG 546  
Db 487 GVKEGDVTNVAQLKGAQNLNRRIDNVGNRAGIAQAIATAGLVQAYLPGKSMMAIGGG 546

Db 487 GVKEGDVTNVAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGG 546

Qy 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
|||||

Db 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591

RESULT 4

US-09-669-974-11

; Sequence 11, Application US/09669974

; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; PRIOR FILING DATE: 2000-09-26

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-11

Query Match 88.8%; Score 525; DB 4; Length 591;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTAVAVLIVNSDKGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTFT 126  
|||||

Db 67 RTAVAVLIVNSDKGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTFT 126  
|||||

Qy 127 YSLKKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186  
|||||

Db 127 YSLKKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186  
|||||

Qy 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRYTDT 246  
|||||

Db 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRYTDT 246  
|||||

Qy 247 VEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDGKLVTKGDKGENSGSTDEGEG 306  
|||||

Db 247 VEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDGKLVTKGDKGENSGSTDEGEG 306  
|||||

Qy 307 LVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASGKGTATVSKDDQG 366  
|||||

Db 307 LVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASGKGTATVSKDDQG 366  
|||||

Qy 367 NITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGN 426  
|||||

Db 367 NITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGN 426  
|||||

Qy 427 NIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKMDPVRTNVP 486  
|||||

Db 427 NIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKMDPVRTNVP 486  
|||||

Qy 487 GVKEGDVTNVAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGG 546  
|||||

Db 487 GVKEGDVTNVAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGG 546  
|||||

Qy 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
|||||

Db 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
|||||

RESULT 5

US-09-377-155-2

; Sequence 2, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 592

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-2

Query Match 73.1%; Score 432; DB 4; Length 592;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 59 DLYLDPVQRTVAVLIVNSDKGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118  
|||||

Db 60 DLYLDPVQRTVAVLIVNSDKGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 119  
|||||

Qy 119 KONGTFTYSLKKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVH 178  
|||||

Db 120 KONGTFTYSLKKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVH 179  
|||||

Qy 179 LINGISTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNV 238  
|||||

Db 180 LINGISTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNV 239  
|||||

Qy 239 DFVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDGKLVTKGDKGENG 298  
|||||

Db 240 DFVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDGKLVTKGDKGENG 299  
|||||

Qy 299 SSTDEGGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASGKGT 358  
|||||

Db 300 SSTDEGGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASGKGT 359  
|||||

Qy 359 TVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD 418  
|||||

Db 360 TVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD 419  
|||||

Qy 419 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNK 478  
|||||

Db 420 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNK 479  
|||||

Qy 479 VRITWAVPGVEGDVTNVAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQAYLP 538  
|||||

Db 480 VRITWAVPGVEGDVTNVAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQAYLP 539  
|||||

Qy 539 SMAIIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
|||||

Db 540 SMAIIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 592  
|||||

RESULT 6

US-09-669-974-2

; Sequence 2, Application US/09669974

; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 73.1%; Score 432; DB 4; Length 592;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 59 DLYLDPVQRTVAVLIIVNSDKETGKEKEVEENSDWYFNEKGVLTAREITLKAGDNLI 118  
DB 60 DLYLDPVQRTVAVLIIVNSDKETGKEKEVEENSDWYFNEKGVLTAREITLKAGDNLI 119  
QY 119 KQNGTNPYSLKADLTDLTSVGTKEKLSFSANGKNVNIITSDTKGLNFAKETAGTNGDTTVH 178  
DB 120 KQNGTNPYSLKADLTDLTSVGTKEKLSFSANGKNVNIITSDTKGLNFAKETAGTNGDTTVH 179  
QY 179 LKNGTSLTDLTLNGATNTVNDVNDDEKRAASVKDVLNAGNVIKGVKPGTASDNV 238  
DB 180 LKNGTSLTDLTLNGATNTVNDVNDDEKRAASVKDVLNAGNVIKGVKPGTASDNV 239  
QY 239 DFVNTYDVEFASDTKTTVNVESKNGKTEVKIGAKTSVIEKDKGLVTGDKDGENG 298  
DB 240 DFVNTYDVEFASDTKTTVNVESKNGKTEVKIGAKTSVIEKDKGLVTGDKDGENG 299  
QY 299 SSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSNTVTFASGKTGA 358  
DB 300 SSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSNTVTFASGKTGA 359  
QY 359 TVSKDDGNTVMYDVGDLNVLNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKDE 418  
DB 360 TVSKDDGNTVMYDVGDLNVLNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKDE 419  
QY 419 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKP 478  
DB 420 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKP 479  
QY 479 VRITNAPGVKGGDVNTVAQLKGVQNLNNDVNDGNARAGIAQAIATAGLVQAYLPK 538  
DB 480 VRITNAPGVKGGDVNTVAQLKGVQNLNNDVNDGNARAGIAQAIATAGLVQAYLPK 539  
QY 539 SMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 591  
DB 540 SMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 592

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 27.2%; Score 161; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 3.9e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 304 GEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSNTVTFASGKTGA 363  
DB 306 GEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSNTVTFASGKTGA 365  
QY 364 DQGNITVMYDVGDLNVLNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKDETVNIN 423  
DB 366 DQGNITVMYDVGDLNVLNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKDETVNIN 425  
QY 424 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 464  
DB 426 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 466

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 27.2%; Score 161; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 3.5e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 304 GEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSNTVTFASGKTGA 363  
DB 306 GEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFETVTSNTVTFASGKTGA 365  
QY 364 DQGNITVMYDVGDLNVLNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKDETVNIN 423  
DB 366 DQGNITVMYDVGDLNVLNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKDETVNIN 425  
QY 424 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 464

Db 426 AGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSD 466

## RESULT 9

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 19.8%; Score 117; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TVHLNGIGSTLTDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIGVKPGTTAS 235

Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIGVKPGTTAS 237

Qy 236 DNVDFVRYDYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292

Db 238 DNVDFVRYDYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 294

## RESULT 10

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 19.8%; Score 117; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TVHLNGIGSTLTDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIGVKPGTTAS 235

Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIGVKPGTTAS 237

Qy 236 DNVDFVRYDYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292

Db 238 DNVDFVRYDYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 294

## RESULT 11

US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 19.8%; Score 117; DB 4; Length 598;

Best Local Similarity 100.0%; Pred. No. 1.6e-102;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TVHLNGIGSTLTDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIGVKPGTTAS 235

Db 182 TVHLNGIGSTLTDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIGVKPGTTAS 241

Qy 236 DNVDFVRYDYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292

Db 242 DNVDFVRYDYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 298

## RESULT 12

US-09-669-974-13  
; Sequence 13, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

```
Query Match          19.6%; Score 117; DB 4; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.6e-102; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TVHLNGIGSLTDLTLNTGATTNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTTAS 235
Db 182 TVHLNGIGSLTDLTLNTGATTNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTTAS 241
Qy 236 DNVDFVRTYDTVEFLSADTKTTTVNVSCKONGKKTVEVKIGAKTSVIKEKDKLVTKG 292
Db 242 DNVDFVRTYDTVEFLSADTKTTTVNVSCKONGKKTVEVKIGAKTSVIKEKDKLVTKG 298

RESULT 13
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match          19.6%; Score 116; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 1.5e-101; Indels 0; Gaps 0;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 476 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNDRVDGNARAGIAQAIAATAGLVQAYL 535
Db 484 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNDRVDGNARAGIAQAIAATAGLVQAYL 543
Qy 536 PGKSMAIGGGTYRGEAGYATGYSSISDGGNWIITKTASNSRGHFGASASVGYQW 591
Db 544 PGKSMAIGGGTYRGEAGYATGYSSISDGGNWIITKTASNSRGHFGASASVGYQW 599

RESULT 14
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; CURRENT APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match          19.8%; Score 117; DB 4; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.6e-102; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TVHLNGIGSLTDLTLNTGATTNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTTAS 235
Db 182 TVHLNGIGSLTDLTLNTGATTNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTTAS 241
Qy 236 DNVDFVRTYDTVEFLSADTKTTTVNVSCKONGKKTVEVKIGAKTSVIKEKDKLVTKG 292
Db 242 DNVDFVRTYDTVEFLSADTKTTTVNVSCKONGKKTVEVKIGAKTSVIKEKDKLVTKG 298

RESULT 13
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match          19.6%; Score 116; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 1.5e-101; Indels 0; Gaps 0;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 476 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNDRVDGNARAGIAQAIAATAGLVQAYL 535
Db 484 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNDRVDGNARAGIAQAIAATAGLVQAYL 543
Qy 536 PGKSMAIGGGTYRGEAGYATGYSSISDGGNWIITKTASNSRGHFGASASVGYQW 591
Db 544 PGKSMAIGGGTYRGEAGYATGYSSISDGGNWIITKTASNSRGHFGASASVGYQW 599

RESULT 14
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; CURRENT APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15
```

```
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match          19.6%; Score 116; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 1.5e-101; Indels 0; Gaps 0;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 476 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNDRVDGNARAGIAQAIAATAGLVQAYL 535
Db 484 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNDRVDGNARAGIAQAIAATAGLVQAYL 543
Qy 536 PGKSMAIGGGTYRGEAGYATGYSSISDGGNWIITKTASNSRGHFGASASVGYQW 591
Db 544 PGKSMAIGGGTYRGEAGYATGYSSISDGGNWIITKTASNSRGHFGASASVGYQW 599

RESULT 15
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17

Query Match          17.4%; Score 103; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 3e-89; Indels 0; Gaps 0;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 LLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEF 249
Db 190 LLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEF 249
Qy 250 LSADTKTTTVNVSCKONGKKTVEVKIGAKTSVIKEKDKLVTKG 292
Db 250 LSADTKTTTVNVSCKONGKKTVEVKIGAKTSVIKEKDKLVTKG 292

Search completed: September 5, 2002, 10:32:33
Job time: 260 sec
```



---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:33:11 ; Search time 33.86 Seconds  
(without alignments)  
1677.165 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNARVAVS.....TASGNSRGHFGASASVGYOW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues  
Word size : 15

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	97.0	591	2	G81133
2	137	23.2	592	2	A81888
					adhesin NMB0992 [i probable surface f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizsa, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TET>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match 97.0%; Score 573; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 VSELTRNHTKRASATVKTAVLATLLPATVQASANNEEQEEDLYLDPVQRTAVVLVNSDK 78  
|||||  
Db 19 VSELTRNHTKRASATVKTAVLATLLPATVQASANNEEQEEDLYLDPVQRTAVVLVNSDK 78  
|||||

Qy 79 EGTGKEKEVEENSNAVFNEKGVLTAREITLKAGDNLIKONGTFTYSLAKDLDLTS 138  
|||||  
Db 79 EGTGKEKEVEENSNAVFNEKGVLTAREITLKAGDNLIKONGTFTYSLAKDLDLTS 138  
|||||

Qy 139 VGTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLTNGATTN 198  
|||||  
Db 139 VGTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLTNGATTN 198  
|||||

Qy 199 VTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDVVEFLSADTKT 258  
|||||  
Db 199 VTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDVVEFLSADTKT 258  
|||||

Qy 259 NVVESKDNGKTEVKIGAKTSVIKEKOGKLVTKDKGNGSSTDEGGLVTAKEVIDAVN 318  
|||||  
Db 259 NVVESKDNGKTEVKIGAKTSVIKEKOGKLVTKDKGNGSSTDEGGLVTAKEVIDAVN 318  
|||||

Qy 319 KAGWRMKTTTANGQTQADKFEVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVGD 378  
|||||  
Db 319 KAGWRMKTTTANGQTQADKFEVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVGD 378  
|||||

Qy 379 ALNVNQLONGSNWNLDSKAVAGSSGVISGNVSPSKGKMDVTNINAGNIEITRNGKNID 438  
|||||  
Db 379 ALNVNQLONGSNWNLDSKAVAGSSGVISGNVSPSKGKMDVTNINAGNIEITRNGKNID 438  
|||||

Qy 439 TATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDNKPVRITNVAPGVKSGDVTNVAQ 498  
|||||  
Db 439 TATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDNKPVRITNVAPGVKSGDVTNVAQ 498  
|||||

Qy 499 LKGVQAQNLNLRIDNDGNARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIGY 558  
|||||  
Db 499 LKGVQAQNLNLRIDNDGNARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIGY 558  
|||||

Qy 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
|||||  
Db 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
|||||

RESULT 2  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match 23.2%; Score 137; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.8e-131;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 KGENGSSTDEGGLVTAKEVIDAVNKGWRMKTTTTANGQTQADKFEVTSGTNVTFASG 353  
|||||

Db 294 KGENGSTDEGECLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFEVTSCTNVTFASG 353  
Qy 354 KGTATVSKDDOGNITVWYDYNVGDALNVNOLONGWNLDSKAVAGSSCKVISGNVSPSK 413  
Db 354 KGTATVSKDDOGNITVWYDYNVGDALNVNOLONGWNLDSKAVAGSSCKVISGNVSPSK 413  
Qy 414 GKWDETIVNINAGNNIEI 430  
Db 414 GKWDETIVNINAGNNIEI 430

Search completed: September 5, 2002, 10:33:11  
Job time: 208 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:39:36 ; Search time 19.19 Seconds  
(without alignments)  
1192.457 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNAWVVS.....TASGNSRGHFGASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
---------------	-------	----------------	--------	-------	-------------

No matches found

Search completed: September 5, 2002, 10:39:36  
Job time: 418 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:39:11 ; Search time 55.9 Seconds  
(without alignments)  
1828.980 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNARVVS.....TAGNSRGHFGASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 15

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_podent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	97.0	591	16 Q9JRI8	Q9JRI8 neisseria m
2	556	94.1	591	2 Q9JPS7	Q9JPS7 neisseria m
3	525	88.8	591	2 Q93QX3	Q93QX3 neisseria m
4	432	73.1	592	2 Q9AQFO	Q9AQFO neisseria m
5	220	37.2	526	2 Q9JPS4	Q9JPS4 neisseria m
6	220	37.2	530	2 Q9JPS1	Q9JPS1 neisseria m
7	195	33.0	594	2 Q9JPI3	Q9JPI3 neisseria m
8	195	33.0	594	2 Q9JPS2	Q9JPS2 neisseria m
9	174	29.4	592	2 Q9JPS9	Q9JPS9 neisseria m
10	171	28.9	598	2 Q9JPR7	Q9JPR7 neisseria m
11	171	28.9	599	2 Q9JPS8	Q9JPS8 neisseria m
12	161	27.2	590	2 Q9JPS3	Q9JPS3 neisseria m
13	161	27.2	594	2 Q93QV4	Q93QV4 neisseria m
14	137	23.2	592	16 Q9JQW4	Q9JQW4 neisseria m
15	117	19.8	594	2 Q9JPH7	Q9JPH7 neisseria m
16	117	19.8	598	2 Q9JPR9	Q9JPR9 neisseria m

17	117	19.8	598	2	Q9JPS0	Q9JPS0 neisseria m
18	116	19.6	599	2	Q9JPR8	Q9JPR8 neisseria m
19	116	19.6	600	2	Q9JPS6	Q9JPS6 neisseria m
20	116	19.6	600	2	Q9JPS5	Q9JPS5 neisseria m
21	103	17.4	592	2	Q93QY2	Q93QY2 neisseria m
22	93	15.7	589	2	Q9JPI0	Q9JPI0 neisseria m
23	93	15.7	589	2	Q93QY1	Q93QY1 neisseria m
24	93	15.7	595	2	Q9JPH0	Q9JPH0 neisseria m
25	93	15.7	598	2	Q9JPT0	Q9JPT0 neisseria m
26	93	15.7	598	2	Q93QV5	Q93QV5 neisseria m
27	19	3.2	1098	2	O48152	O48152 haemophilus
28	18	3.0	2353	2	P71401	P71401 haemophilus

#### ALIGNMENTS

```
RESULT 1
Q9JRI8 ID Q9JRI8 PRELIMINARY: PRT; 591 AA.
AC Q9JRI8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
DE PROTEIN).
GN GNA992 OR NMB0992 OR NHHA.
OS Neisseria meningitidis, and
OC Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Cittoni H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SPECIES=N meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -
DR EMBL; AF002450; AAF41395.1; -
DR EMBL; AF226367; AAF42516.1; -
DR EMBL; AF226370; AAF42519.1; -
DR EMBL; AF226374; AAF42523.1; -
DR EMBL; AF157611; AAK68872.1; -
```

DR TIGR: NM00992; --  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73BC6 CRC64;

Query Match 97.0%; Score 573; DB 16; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELTNRHTRKASATVKTAVLATLLFATVQASANNBEEDELYLDPVQRTAVLVNSDK 78  
DB 19 VSELTNRHTRKASATVKTAVLATLLFATVQASANNBEEDELYLDPVQRTAVLVNSDK 78

QY 79 EGTGEKEKVEENSDWAVYFNKGVLTAREITLKAGDNLIKQNGNFTYSLKKDLTDLTS 138  
DB 79 EGTGEKEKVEENSDWAVYFNKGVLTAREITLKAGDNLIKQNGNFTYSLKKDLTDLTS 138

QY 139 VGTKEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDLLNLTGATN 198  
DB 139 VGTKEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDLLNLTGATN 198

QY 199 VTNDNVTDDKKRAASVXKDVNLNAGNITKGVKPGTTASDNVDVRYDTVEFLSADTKTTT 258  
DB 199 VTNDNVTDDKKRAASVXKDVNLNAGNITKGVKPGTTASDNVDVRYDTVEFLSADTKTTT 258

QY 259 VNVEKDNKGKTEVKIGARTSVIKKDKGLVTKGDKGNGSSTDEGEGLVTAKEVIDAVN 318  
DB 259 VNVEKDNKGKTEVKIGARTSVIKKDKGLVTKGDKGNGSSTDEGEGLVTAKEVIDAVN 318

QY 319 KAGWRMKTITANGQTQADKPEVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
DB 319 KAGWRMKTITANGQTQADKPEVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378

QY 379 ALNVNQLONGNLDKAVAGSSGKVLISGNVSPSKGMDETVNIAGNNIETTRNGKID 438  
DB 379 ALNVNQLONGNLDKAVAGSSGKVLISGNVSPSKGMDETVNIAGNNIETTRNGKID 438

QY 439 IATSMPPORSSVSLGADAPTLSDGDNALVSKKDKPVRITNVAPGVKEGDTVNAQ 498  
DB 439 IATSMPPORSSVSLGADAPTLSDGDNALVSKKDKPVRITNVAPGVKEGDTVNAQ 498

QY 499 LKGAQNANLRINDVGNARAGIAQATATAGLVQAYLPKSKMAIGGGTYRGEAGYAGY 558  
DB 499 LKGAQNANLRINDVGNARAGIAQATATAGLVQAYLPKSKMAIGGGTYRGEAGYAGY 558

QY 559 SSISDGGNWTIKGTASGNSRHFAGASASVGYQW 591  
DB 559 SSISDGGNWTIKGTASGNSRHFAGASASVGYQW 591

## RESULT 2

Q9JPS7  
ID Q9JPS7 PRELIMINARY; PRT; 591 AA.  
AC Q9JPS7  
DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Maignani V., Gullani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1; --  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 94.1%; Score 556; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TAVLATLLFATVQASANNBEEDELYLDPVQRTAVLVNSDKCEKCEKVEENSDWAV 95  
DB 36 TAVLATLLFATVQASANNBEEDELYLDPVQRTAVLVNSDKCEKCEKVEENSDWAV 95

QY 96 YFNEKGVLTAREITLKAGDNLIKQNGNFTYSLKKDLTDLTSVGTKEKLSFSAANGKVN 155  
DB 96 YFNEKGVLTAREITLKAGDNLIKQNGNFTYSLKKDLTDLTSVGTKEKLSFSAANGKVN 155

QY 156 TSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDLLNLTGATNVTNDNVTDDKKRAASV 215  
DB 156 TSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDLLNLTGATNVTNDNVTDDKKRAASV 215

QY 216 KDVLNAGNITKGVKPGTTASDNVDVRYDTVEFLSADTKTTVNVESKDNKGKTEVKIG 275  
DB 216 KDVLNAGNITKGVKPGTTASDNVDVRYDTVEFLSADTKTTVNVESKDNKGKTEVKIG 275

QY 276 AKTSVKEKDKGLVTKGDKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQ 335  
DB 276 AKTSVKEKDKGLVTKGDKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQ 335

QY 336 ADKFEVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGNALVNSQLONGNLDK 395  
DB 336 ADKFEVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGNALVNSQLONGNLDK 395

QY 396 AVAGSSGKVLISGNVSPSKGMDETVNIAGNNIETTRNGKIDIASMTPPQSSVSLGAG 455  
DB 396 AVAGSSGKVLISGNVSPSKGMDETVNIAGNNIETTRNGKIDIASMTPPQSSVSLGAG 455

QY 456 ADAPTLSDGDNALVSKKDKPVRITNVAPGVKEGDTVNAQKGAQNANLRINDVNDG 515  
DB 456 ADAPTLSDGDNALVSKKDKPVRITNVAPGVKEGDTVNAQKGAQNANLRINDVNDG 515

QY 516 NARAGIAQATATAGLVQAYLPKSKMAIGGGTYRGEAGYAGYSSISDGGNWTIKGTASG 575  
DB 516 NARAGIAQATATAGLVQAYLPKSKMAIGGGTYRGEAGYAGYSSISDGGNWTIKGTASG 575

QY 576 NSRGHFGASASVGYQW 591  
DB 576 NSRGHFGASASVGYQW 591

## RESULT 3

Q93QY3  
ID Q93QY3 PRELIMINARY; PRT; 591 AA.  
AC Q93QY3  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RA "Identification and characterization of a gene encoding a novel outer  
RA membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157606; AAK68867.1; --  
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;



```
Query Match      88.8%; Score 525; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTAVAVLIVNSDKGTGEKEKYEENSQWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFT 126
Db 67 RTAVAVLIVNSDKGTGEKEKYEENSQWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFT 126

Qy 127 YSLKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTTHLNGIGSTL 186
Db 127 YSLKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTTHLNGIGSTL 186

Qy 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIKVPGTGTASDNVDFVRYDT 246
Db 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIKVPGTGTASDNVDFVRYDT 246

Qy 247 VEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGDKGNGSSSTDEGEG 306
Db 247 VEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGDKGNGSSSTDEGEG 306

Qy 307 LVTAKEVIDAYNKAGWRMKTTTANGOTGOADKFETVTSCTNVTTFASGKGTATYSKDDQG 366
Db 307 LVTAKEVIDAYNKAGWRMKTTTANGOTGOADKFETVTSCTNVTTFASGKGTATYSKDDQG 366

Qy 367 NITVMYDVGDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMDETVNNAGN 426
Db 367 NITVMYDVGDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMDETVNNAGN 426

Qy 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVAQIAIATAGLVQAYLPKG 486
Db 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVAQIAIATAGLVQAYLPKG 486

Qy 487 GYKEDVTNVAQLKGVAQNLRNDVNGNARAGIAQIAIATAGLVQAYLPKGSMMAIGGG 546
Db 487 GYKEDVTNVAQLKGVAQNLRNDVNGNARAGIAQIAIATAGLVQAYLPKGSMMAIGGG 546

Qy 547 TYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 591
Db 547 TYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 591

RESULT 4
Q9AQF0 ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikanta Y., Dieckelmann M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match      73.1%; Score 432; DB 2; Length 592;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 59 DLYLDPVQRTVAVLIVNSDKGTGEKEKYEENSQWAVYFNEKGVLTAREITLKAGDNLKI 118
Db 60 DLYLDPVQRTVAVLIVNSDKGTGEKEKYEENSQWAVYFNEKGVLTAREITLKAGDNLKI 119
```

```
Qy 119 KQNGTFTYSLKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTTH 178
Db 120 KQNGTFTYSLKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTTH 179

Qy 179 LNGIGSTLTDPLLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIKVPGTGTASDNV 238
Db 180 LNGIGSTLTDPLLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIKVPGTGTASDNV 239

Qy 239 DFVETVDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGDKGNG 298
Db 240 DFVETVDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGDKGNG 299

Qy 299 SSTDEGEGLVTAKEVIDAYNKAGWRMKTTTANGOTGOADKFETVTSCTNVTTFASGKGT 358
Db 300 SSTDEGEGLVTAKEVIDAYNKAGWRMKTTTANGOTGOADKFETVTSCTNVTTFASGKGT 359

Qy 359 TVSKDDOGNITVMYDVGDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMD 418
Db 360 TVSKDDOGNITVMYDVGDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMD 419

Qy 419 TVNNAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKP 478
Db 420 TVNNAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKP 479

Qy 479 VRITNVPVGVKEGDTNVAQLKGVAQNLRNDVNGNARAGIAQIAIATAGLVQAYLPKG 538
Db 480 VRITNVPVGVKEGDTNVAQLKGVAQNLRNDVNGNARAGIAQIAIATAGLVQAYLPKG 539

Qy 539 SMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 591
Db 540 SMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 592

RESULT 5
Q9JPS4 ID Q9JPS4 PRELIMINARY; PRT; 526 AA.
AC Q9JPS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG6/88;
RA Piazza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nulì S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226377; AAF42526.1; -.
SQ SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;

Query Match      37.2%; Score 220; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 YDVMYGDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMDETVNNAGNNIEIT 431
Db 307 YDVMYGDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMDETVNNAGNNIEIT 366

Qy 432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKPVRITNVPVKEG 491
```

|||||  
Db 367 RKGKNDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKDKNKPVRITNVAPGVKEG 426  
QY 492 DVTNVAQLKGVQVGNLNRIDNVGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYRGE 551  
Db 427 DVTNVAQLKGVQVGNLNRIDNVGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYRGE 486  
QY 552 AGYAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 591  
Db 487 AGYAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 526  
RESULT 6  
Q9JPS1 PRELIMINARY; PRT: 530 AA.  
AC Q9JPS1  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGF26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226380; AAF42529.1; -.  
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;

Query Match 37.2%; Score 220; DB 2; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.3e-203;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 372 YDVNVGDLNVLQNSGNLDSKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIET 431  
Db 311 YDVNVGDLNVLQNSGNLDSKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIET 370  
QY 432 RKGKNDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKDKNKPVRITNVAPGVKEG 491  
Db 371 RKGKNDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKDKNKPVRITNVAPGVKEG 430  
QY 492 DVTNVAQLKGVQVGNLNRIDNVGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYRGE 551  
Db 431 DVTNVAQLKGVQVGNLNRIDNVGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYRGE 490  
QY 552 AGYAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 591  
Db 491 AGYAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 530  
RESULT 7  
Q9JPI3 PRELIMINARY; PRT: 594 AA.  
AC Q9JPI3  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88; AND B232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -.  
DR EMBL: AF226369; AAF42518.1; -.  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D04B46 CRC64;  
Query Match 33.0%; Score 195; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 3.3e-179;  
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 152 KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLTNGATTNVDNVTDEKKR 211  
Db 154 KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLTNGATTNVDNVTDEKKR 213  
QY 212 AASVKVDVNLGNWIKVKGPTASDNVDFVITYDTVFELFSLADTKTTVNVEKDKNGKTE 271  
Db 214 AASVKVDVNLGNWIKVKGPTASDNVDFVITYDTVFELFSLADTKTTVNVEKDKNGKTE 273  
QY 272 VKIGAKTSVKEKDKGLVTGDKGNGSGSTDEGGLVTAKEVIDAVNKAGWRMKTITANG 331  
Db 274 VKIGAKTSVKEKDKGLVTGDKGNGSGSTDEGGLVTAKEVIDAVNKAGWRMKTITANG 333  
QY 332 QTGOADKFEFVTSGT 346  
Db 334 QTGOADKFEFVTSGT 348  
RESULT 8  
Q9JPS2 PRELIMINARY; PRT: 594 AA.  
AC Q9JPS2  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -.  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;  
Query Match 33.0%; Score 195; DB 2; Length 594;

Best Local Similarity	100.0%;	Pred. NO. 3.3e-179;			
Matches	195;	Conservative	0;	Mismatches	0;
Indels			0;		
Gaps					
0;					
QY	152	KVNITSDTKGINFAKEAGTAGNGD	TVHLNGIGSTLTDTLLTGAT	TNTVNDVTDDEKKR	211
Db	154	KVNITSDTKGLNFAKETAGTNGD	TVHLNGIGSTLTDTLLTGAT	TNTVNDVTDDEKKR	213
QY	212	AASVKDVLNAGWNKGVKPGT	TASDNVDVFRVYDTVFELSAD	TKTTVNVESKONGKKTE	271
Db	214	AASVKDVLNAGWNKGVKPGT	TASDNVDVFRVYDTVFELSAD	TKTTVNVESKONGKKTE	273
QY	272	VKTGAKTSVTKEDGKLVTKD	KGENGSSTDEGGLVTAK	EIDAVNKGARMKTTTANG	331
Db	274	VKTGAKTSVTKEDGKLVTKD	KGENGSSTDEGGLVTAK	EIDAVNKGARMKTTTANG	333
QY	332	QTGQADKFEETVTSQT	346		
Db	334	QTGQADKFEETVTSQT	348		
RESULT	9				
Q9JPS9					
ID	Q9JPS9	PRELIMINARY;	PRT;	592 AA.	
AC	Q9JPS9;				
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)				
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=860800;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santoli L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.				
RT	"Identification of Vaccine Candidates Against Serogroup B				
RT	Meningococcus by Whole-Genome Sequencing."				
RL	Science 287:1816-1820(2000).				
EMBL	AF226361; AAF42510.1; .				
SR	SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;				

Query Match	29.4%	Score 174;	DB 2;	Length 592;
Best Local Similarity	99.6%;	Pred. No. 5.9e-159;		
Matches 274;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	190	LLNTGATTNTNDNVTDDEKKRAASVDVLNAGNWIKGVKPGTTSASDNVDVFRYDTVEF	249	
Db	190	LLNTGATTNTNDNVTDDEKKRAASVDVLNAGNWIKGVKPGTTSASDNVDVFRYDTVEF	249	
QY	250	LSADTKTTTVNVESKDNKGKTEVKGIGAKTSVIEKDKGLVTGKDKGENSGSTDEGEGLVT	309	
Db	250	LSADTKTTTVNVESKDNKGKTEVKGIGAKTSVIEKDKGLVTGKDKGENSGSTDEGEGLVT	309	
QY	310	AKEVIDAVNKGWRMKTITANGQTQADKFTVTSCTNVTFASGKGTTATYSKDDQGNIT	369	
Db	310	AKEVIDAVNKGWRMKTITANGQTQADKFTVTSCTNVTFASGKGTTATYSKDDQGNIT	369	
QY	370	VMYDVNVGDALNVQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGMDETYNINAGNNIE	429	
Db	370	VMYDVNVGDALNVQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGMDETYNINAGNNIE	429	
QY	430	ITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDV	464	
Db	430	ITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDV	464	

RESULT	ID	Q5JPR7	PRELIMINARY;	PRT;	598 AA.
Q9JPR7	ID	Q5JPR7	PRELIMINARY;	PRT;	598 AA.
AC	Q5JPR7	AC	Q5JPR7	PRT;	598 AA.
DT	01-OCT-2000	(TREMBlrel. 15, Created)			
DT	01-OCT-2000	(TREMBlrel. 15, Last sequence update)			
DT	01-MAR-2001	(TREMBlrel. 16, Last annotation update)			
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SWZ107;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.;				
RT	Identification of Vaccine Candidates Against Serogroup B				
RT	Meningococcus by whole-Genome Sequencing."				
RL	Science 287:1816-1820(2000).				
DR	EMBL; AF226385; AAF42534.1; -				
SQ	SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;				
Query Match	28.9%;	Score 171;	DB 2;	Length 598;	
Best Local Similarity	100.0%;	Pred No. 4.7e-156;			
Matches 171;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	294	KGEGSSTDEGEGLVTAKEVIDAYNKAGWRMKTTTANGQTQADKFEVTVSGTNVTFASG 353			
Db	300	KGEGSSTDEGEGLVTAKEVIDAYNKAGWRMKTTTANGQTQADKFEVTVSGTNVTFASG 359			
QY	354	KGTTATVSKDDQGNITVMYDYNVGDNALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 413			
Db	360	KGTTATVSKDDQGNITVMYDYNVGDNALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 419			
QY	414	GKMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLISVD 464			
Db	420	GKMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLISVD 470			
RESULT 11					
Q9JPS8	ID	Q5JPS8	PRELIMINARY;	PRT;	599 AA.
AC	Q5JPS8	AC	Q5JPS8	PRT;	599 AA.
DT	01-OCT-2000	(TREMBlrel. 15, Created)			
DT	01-OCT-2000	(TREMBlrel. 15, Last sequence update)			
DT	01-MAR-2001	(TREMBlrel. 16, Last annotation update)			
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A22;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.;				
RT	Identification of Vaccine Candidates Against Serogroup B				

RT Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226364; AAF42513.1; -.  
 SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 28.9%; Score 171; DB 2; Length 599;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-156;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 KGENGSTDEGELVTAKEVIDAVNKGAWRKMTTANGOTGQADKFETVTSNTVTFASG 353  
 Db 301 KGENGSTDEGELVTAKEVIDAVNKGAWRKMTTANGOTGQADKFETVTSNTVTFASG 360  
 Qy 354 KGTATVSKDDOGNITVYDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSK 413  
 Db 361 KGTATVSKDDOGNITVYDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSK 420  
 Qy 414 GKMDVNTNAGNNEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSD 464  
 Db 421 GKMDVNTNAGNNEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSD 471

RESULT 12

Q9JFS3 ID Q9JFS3 PRELIMINARY; PRT; 590 AA.  
 AC Q9JFS3;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCE28;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Camanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Masotti T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon R., Grand G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226378; AAF42527.1; -.  
 SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 27.2%; Score 161; DB 2; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-146;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 ITLKAGDNLIKQNGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKE 167  
 Db 106 ITLKAGDNLIKQNGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKE 165  
 Qy 168 TACTNGDTTVHLNGISLTITLTLTGATNTVNDVTDDEKKRAASKVDVNLGAGNWK 227  
 Db 166 TACTNGDTTVHLNGISLTITLTLTGATNTVNDVTDDEKKRAASKVDVNLGAGNWK 225  
 Qy 228 VKPGTTASNDVDFVTVDFELSDTKTTVANVESKDNK 268  
 Db 226 VKPGTTASNDVDFVTVDFELSDTKTTVANVESKDNK 266

RESULT 13

Q93QY4 ID Q93QY4 PRELIMINARY; PRT; 594 AA.

AC Q93QY4;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EG327;  
 RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of Neisseria meningitidis."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157605; AAK68866.1; -.  
 SQ SEQUENCE 594 AA; 62297 MW; 9DD448B04B3A8EA2 CRC64;

Query Match 27.2%; Score 161; DB 2; Length 594;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-146;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 GEGLVTAKEVIDAVNKGAWRKMTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 363  
 Db 306 GEGLVTAKEVIDAVNKGAWRKMTTANGOTGQADKFETVTSNTVTFASGKGTATVSKD 365  
 Qy 364 DQGNITVYDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSKMDVNTV 423  
 Db 366 DQGNITVYDVNVGDALNVQNSGNWLDKAVAGSSGKVISGNVSPSKMDVNTV 425  
 Qy 424 AGNNEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSD 464  
 Db 426 AGNNEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSD 466

RESULT 14

Q9JQW4 ID Q9JQW4 PRELIMINARY; PRT; 592 AA.  
 AC Q9JQW4;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE PUTATIVE SURFACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).  
 GN NHA1200 OR GNA992.  
 OS Neisseria meningitidis (serogroup A), and  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65699, 487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;  
 RX MEDLINE=2022556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,  
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrall B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria  
 meningitidis 22491".  
 RL Nature 404:502-506(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=205900; B6133, F6124, AND 22491;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Masotti T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RL Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AL162755; CAB84461.1; -  
DR EMBL; AF226357; AAF42506.1; -  
DR EMBL; AF226365; AAF42514.1; -  
DR EMBL; AF226373; AAF42522.1; -  
DR EMBL; AF226386; AAF42535.1; -  
KW Complete proteome.  
SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match 23.2%; Score 137; DB 16; Length 592;  
Best Local Similarity 100.0%; Pred. No. 2.9e-123;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KGEGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFETVTSNTVTFASG 353  
DB 294 KGEGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFETVTSNTVTFASG 353  
QY 354 KGTATVSKDQGNITVMDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSK 413  
DB 354 KGTATVSKDQGNITVMDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSK 413  
QY 414 GKMDETVINAGNNIEI 430  
DB 414 GKMDETVINAGNNIEI 430

## RESULT 15

Q9JPH7  
ID Q9JPH7 PRELIMINARY; PRT; 594 AA.  
AC Q9JPH7;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198, AND 297-0;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzo M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198;  
RA Peak I.R., Srikhanta Y., Dieckelmann M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF226368; AAF42517.1; -  
DR EMBL; AF226358; AAF42507.1; -  
DR EMBL; AF157604; AAK68865.1; -  
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 19.8%; Score 117; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 5.8e-104;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTAS 235  
DB 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTAS 237  
QY 236 DNVDVFRVTDVVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDGKLVTK 292  
DB 236 DNVDVFRVTDVVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDGKLVTK 294  
Search completed: September 5, 2002, 10:39:13  
Job time: 430 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:40:42 ; Search time 58.74 Seconds  
(without alignments)  
1117.545 Million cell updates/sec

Title: US-09-700-293-4

Perfect score: 591

Sequence: 1 MNKIYRIWNSALNAWVAVS.....TASGSRGHFGASVGYQW 591

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 20

Total number of hits satisfying chosen parameters: 37

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_032802.\*

```

1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	97.0	591	20	AA1980
2	573	97.0	591	20	AA1981
3	573	97.0	591	20	AA1982
4	525	88.8	591	22	AA1983
5	525	88.8	591	22	AA1984
6	458	77.5	512	22	AA1985
7	432	73.1	592	20	AA1986
8	381	64.5	433	22	AA1987
9	367	62.1	591	21	AA1988
10	355	60.1	407	22	AA1989
11	355	60.1	502	22	AA1990

12	175	29.6	245	20	AA1980	Amino acid sequence
13	161	27.2	594	20	AA1981	A surface protein
14	161	27.2	594	21	AA1982	BAS029 amino acid
15	161	27.2	594	22	AA1983	N meningitidis EG
16	137	23.2	592	20	AA1984	Amino acid sequence
17	137	23.2	592	22	AA1985	N meningitidis 22
18	117	19.8	594	20	AA1986	A surface protein
19	117	19.8	594	22	AA1987	N meningitidis B2
20	117	19.8	598	20	AA1988	A surface protein
21	117	19.8	598	22	AA1989	N meningitidis H1
22	116	19.6	116	21	AA1990	Neisserial conserv
23	116	19.6	599	20	AA1991	A surface protein
24	116	19.6	599	22	AA1992	N meningitidis H3
25	103	17.4	513	22	AA1993	N meningitidis H4
26	103	17.4	592	20	AA1994	A surface protein
27	103	17.4	592	22	AA1995	N meningitidis H4
28	93	15.7	589	20	AA1996	A surface protein
29	93	15.7	589	22	AA1997	N meningitidis P2
30	93	15.7	598	20	AA1998	A surface protein
31	93	15.7	598	22	AA1999	N meningitidis B2
32	72	12.2	72	21	AA2000	Neisserial conserv
33	59	10.0	604	22	AA2001	N meningitidis su
34	56	9.5	56	21	AA2002	Neisserial conserv
35	53	9.0	53	21	AA2003	Neisserial conserv
36	23	3.9	23	21	AA2004	Neisserial conserv
37	20	3.4	20	21	AA2005	Neisserial conserv

#### ALIGNMENTS

```

RESULT 1
AA1980
ID AAY27202 standard; Protein; 591 AA.
XX AAY27202;
AC AAY27202;
DT 24-SEP-1999 (first entry)
XX Amino acid sequence of N. meningitidis protein ORF40-1.
DE Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX Neisseria meningitidis.
OS WO9336544-A2.
XX 22-JUL-1999.
PD 14-JAN-1999; 99WO-IB00103.
PF 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX (CHIR-) CHIRON SPA.
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
PI WPI; 1999-444400/37.
DR N-PSDB; AAX99124.
XX New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX Claim 1; Page 62; 123pp; English.
XX The invention provides proteins (AAY27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a

```

CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisseria  
CC bacteria, especially Neisseria meningitidis.  
XX  
SQ Sequence 591 AA;

Query Match 97.0%; Score 573; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 VSELRNHTKRASATVKTAVLATLLFATVQASANNEQEDLYLDPVQRTVAVLIIVNSDK 78  
Db 19 vseltrnhtkrasatvktavlatllfatvqasanneegeeelyldpvrvtavliivnsdk 78  
QY 79 EGTGEKEKVEENSDWAVYNEKGVLTAREITLKAGDNLKIKQNGTFTYSLKDKLTDLTS 138  
Db 79 egtgekekeveensdwavynekgvltareitlkagdnlkikqngtftyslkkdltdlts 138  
QY 139 VGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDVTTLHNGIGSTLTDLLNTGATTN 198  
Db 139 vgteklsfsangknvnitsdtkglnfaketagtgdtvthlngigstltdllntgattn 198  
QY 199 VTNDNVTDDEKRAASVKDVLNAGWNIGVKPGTTASDNVDFVRYDTVEFLSADTKTTT 258  
Db 199 vtndnvtddckraasvkavlnagwnikvpgttasdnvdfvrydtvrefilsadtkttt 258  
QY 259 VNVESKDNGKKEVKIGAKTSVIKEKDGKLVTKGDKGENSGSTDEGEGLVTAKEVIDAVN 318  
Db 259 vnveskdngkktevki gaktsvikekdgklytkgdkgensstdegeglvtakev idavn 318  
QY 319 KAGWRMTTANGQTQADKFETVTSNGTNTVFASGKTTATVSKDOGNITVWYDVNVGD 378  
Db 319 kagwrmttcangqtqadkfetvtsngntvfaskgttatvskddqgnitvmydvngvd 378  
QY 379 ALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIEITRNGKNID 438  
Db 379 alnvngqlqnsqwnldskavagssgkvisgnvpsksgkmdetvlnagnnieitrngknid 438  
QY 439 IATSMTPQFSVSLGAGADAPTLSDVDGALNVGSKKDNKPFVITNTVAPGKEGDTVNTAQ 498  
Db 439 iatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpvritntvapgkegdtvntaq 498  
QY 499 LKGVQAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPFGKSMMAIGGTYRGEAGYAGY 558  
Db 499 lkqvaaqnl nrridnvdgnarag iaqaiataglvqaylpgkmmai ggytyrgeagyaigy 558  
QY 559 SSISDGGNWIIGKTASGNSRHFASASVGYQW 591  
Db 559 ssisdggnwiikgtasgnsrghfgasasvgyqw 591

## RESULT 2

AAV23746  
ID AAV23746 standard; Protein; 591 AA.

AC AAV23746;

DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

DE Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX Neisseria meningitidis.

XX WO9931132-A1.

PN 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UIQU ) UNIV QUEENSLAND.  
XX Jennings MP, Moxon ER, Peak IRA;  
PI WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX Claim 1; Page 127-128; 132pp; English.  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;

Query Match 97.0%; Score 573; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELRNHTKRASATVKTAVLATLLFATVQASANNEQEDLYLDPVQRTVAVLIIVNSDK 78  
Db 19 vseltrnhtkrasatvktavlatllfatvqasanneegeeelyldpvrvtavliivnsdk 78  
QY 79 EGTGEKEKVEENSDWAVYNEKGVLTAREITLKAGDNLKIKQNGTFTYSLKDKLTDLTS 138  
Db 79 egtgekekeveensdwavynekgvltareitlkagdnlkikqngtftyslkkdltdlts 138  
QY 139 VGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDVTTLHNGIGSTLTDLLNTGATTN 198  
Db 139 vgteklsfsangknvnitsdtkglnfaketagtgdtvthlngigstltdllntgattn 198  
QY 199 VTNDNVTDDEKRAASVKDVLNAGWNIGVKPGTTASDNVDFVRYDTVEFLSADTKTTT 258  
Db 199 vtndnvtddckraasvkavlnagwnikvpgttasdnvdfvrydtvrefilsadtkttt 258  
QY 259 VNVESKDNGKKEVKIGAKTSVIKEKDGKLVTKGDKGENSGSTDEGEGLVTAKEVIDAVN 318  
Db 259 vnveskdngkktevki gaktsvikekdgklytkgdkgensstdegeglvtakev idavn 318  
QY 319 KAGWRMTTANGQTQADKFETVTSNGTNTVFASGKTTATVSKDOGNITVWYDVNVGD 378  
Db 319 kagwrmttcangqtqadkfetvtsngntvfaskgttatvskddqgnitvmydvngvd 378  
QY 379 ALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIEITRNGKNID 438  
Db 379 alnvngqlqnsqwnldskavagssgkvisgnvpsksgkmdetvlnagnnieitrngknid 438  
QY 439 IATSMTPQFSVSLGAGADAPTLSDVDGALNVGSKKDNKPFVITNTVAPGKEGDTVNTAQ 498  
Db 439 iatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpvritntvapgkegdtvntaq 498  
QY 499 LKGVQAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPFGKSMMAIGGTYRGEAGYAGY 558  
Db 499 lkqvaaqnl nrridnvdgnarag iaqaiataglvqaylpgkmmai ggytyrgeagyaigy 558  
QY 559 SSISDGGNWIIGKTASGNSRHFASASVGYQW 591  
Db 559 ssisdggnwiikgtasgnsrghfgasasvgyqw 591





OS Neisseria meningitidis.  
 PW WO9931132-A1.  
 XX 24-JUN-1999.  
 XX 14-DEC-1998; 98WO-AU01031.  
 XX 12-DEC-1997; 97GB-0026398.  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX (UYQU ) UNIV QUEENSLAND.  
 XX Jennings MP, Moxon ER, Peak IRA;  
 XX WPI: 1999-418754/35.  
 XX DR N-PSDB; AAX85793.  
 XX Neisseria meningitidis surface proteins useful for treating N.  
 XX meningitidis Infections  
 XX Claim 1; Page 104-106; 132pp; English.  
 XX The present sequence represents a surface protein of Neisseria  
 XX meningitidis which is approximately 62 kDa. The N. meningitidis  
 XX surface glycoproteins, nucleic acids, the primers and optionally  
 XX a thermostable polymerase, or antibodies are useful in a kit for  
 XX the detection or diagnosis of N. meningitidis infection in humans.  
 XX The N. meningitidis surface glycoproteins can also be used to  
 XX prevent or treat N. meningitidis infection in humans, especially  
 XX in the form of vaccines. The proteins and antibodies can also  
 XX be used to identify immunoreactive peptides.  
 XX Sequence 591 AA:  
 QY Query Match 88.8%; Score 525; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 67 RTVALVINSDEGTEGKEKEVEENSDMAVFNKGVLTAREITLAKAGDNLKIKONGTFT 126  
 Db 67 rtvalvinsdegtegekeveensdwavfnekgvltareitlkgadnlkikngtft 126  
 QY 127 YSLKDLTDLTSGTEKLSFSAANGKYNITSDTKGLNFAKETAGTNGDTVHLNGIGSTL 186  
 Db 127 yslkdltdltsvgtelksfsaangknvitsdtkglnfaketagtngdttvhlngigstl 186  
 QY 187 TDTLLNTGATTNNVDNDVDEKRAASVQVNLNAGNFKGVKPGTTASDNDVFRYDT 246  
 Db 187 tdtllntgattnnvdndvdekkraasvqvnlnagnfkvgkpgttasdnvdrtydt 246  
 QY 247 VEFLSADTKTTNNVESKDKKTEVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEG 306  
 Db 247 veflsadtkttnnveskdngkktvkgigaktsvkekdkgkltvgdkgengsstdegeg 306  
 QY 307 LVTAKEVIDAVNKAQWRKMTTANGQTQADKFETVTSGTNTVFASGKGTATVSKDDQG 366  
 Db 307 lvtakevidavnakagwrkmtttangtqgqadkfetvtsgtntvfaskgtattvskddqg 366  
 QY 367 NITVMVDVNGDALNVNQLQNSGWNLDKSAVAGSSGKVTSGNVSPSKGMDETVNIAGN 426  
 Db 367 nitvmvdvngdnlvvnqlqnsqwnldskavagssgkvtsgnvspskgmdetvniagn 426  
 QY 427 NIETRNKGNIDIASMTPOFSSVSLGAGADAPTLSDGDLNVGSKDKNKPVRTNNAP 486  
 Db 427 nietrngknidiasmtppofssvslgagadaptlsvdgdlnvsgkdknkpvrtnnap 486  
 QY 487 GVKEGDTNNVAOLKGVANLNRRNDVNGNARAGIAQATATAGLVQAVLPKGSMAITGG 546  
 Db 487 gvkegdtnnvaqlkgvanlnrrndvngnargaragiatataglvqavlpkgsmaia1999 546  
 QY 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

Db 547 tyrgeagyaigysissdggngwiikgtasgnsrghfgasasvgyqw 591  
 RESULT 5  
 ID AAU06175 standard; Protein; 591 AA.  
 XX AAU06175;  
 XX 24-OCT-2001 (first entry)  
 XX N. meningitidis EG329 surface antigen Nhha polypeptide sequence.  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 XX Neisseria meningitidis strain EG329.  
 XX Key Location/Qualifiers  
 XX Region 1..50  
 XX /label= C1  
 XX /note= "Conserved region 1"  
 XX Region 51..108  
 XX /label= V1  
 XX /note= "Variable region 1"  
 XX Region 109..120  
 XX /label= C2  
 XX /note= "Conserved region 2"  
 XX Region 121..124  
 XX /label= V2  
 XX /note= "Variable region 2"  
 XX Region 125..188  
 XX /label= C3  
 XX /note= "Conserved region 3"  
 XX Region 189..210  
 XX /label= V3  
 XX /note= "Variable region 3"  
 XX Region 211..229  
 XX /label= C4  
 XX /note= "Conserved region 4"  
 XX Region 230..236  
 XX /label= V4  
 XX /note= "Variable region 4"  
 XX Region 237..591  
 XX /label= C5  
 XX /note= "Conserved region 5"  
 WO200155182-A1.  
 XX 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-AU00069.  
 XX 25-JAN-2000; 2000US-0177917.  
 XX (UYQU ) UNIV QUEENSLAND.  
 XX Peak IRA, Jennings MP;  
 XX WPI: 2001-488774/53.  
 XX N-PSDB; AAS09165.  
 XX New Nhha surface antigen polypeptides and polynucleotides from  
 XX Neisseria meningitidis, useful in producing vaccines for treating or  
 XX preventing broad spectrum of Neisseria meningitidis -  
 XX Claim 9; Fig 1; 91pp; English.  
 XX The present invention relates to the isolation of novel Neisseria  
 XX meningitidis mutant polypeptides of the surface antigen Nhha  
 XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 XX characterised by deletions of non-conserved amino acids, particularly  
 XX the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen NhhA  
CC from N. meningitidis strain EG329 is 1 of 10 NhhA polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
XX Sequence 591 AA;

Query Match 88.8%; Score 525; DB 22; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTVAVLIVNSDKETGEKEKVEENSDWAVYFNEKGLVTAREITLKAGDNLIKQNGTNT 126  
Db |||||||  
Qy 127 YSLKKDLTLTSVGTKEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186  
Db |||||||  
Qy 187 TDTLINTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYTDT 246  
Db |||||||  
Qy 247 VEFISADTKTTNVNESKDNKKTEVKIGAKTSVKEKDKGLVTKGKGENGSSTDEGEG 306  
Db |||||||  
Qy 307 LVTAKEDVDVAVKAGWRMKTNTANGOTGQADKFEVTSCTNVTASGKGTATVSKDDQG 366  
Db |||||||  
Qy 367 NITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGN 426  
Db |||||||  
Qy 427 NIEITRNKNDIATSMPTQSSVSLGAGADAPTLVSVDGDALNVGSKDKNPVRITNVAP 486  
Db |||||||  
Qy 487 GVKEGDVTNVAQLKGVAQLNLRIDNVGNARAGTAQAIATAGLVQAYLPCKSMMAIGG 546  
Db |||||||  
Qy 547 TYRGEAGYAGYSSISDGGNNRIKGTASGNSRGHFGASVGYQW 591  
Db |||||||

RESULT 6  
AAU06182  
ID AAU06182 standard; Protein; 512 AA.  
XX  
XX AC AAU06182;  
XX DT 24-OCT-2001 (first entry)  
XX DE N. meningitidis PMC21 NhhA deletion mutant #1.  
XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine;  
KW mutant; mutein.  
XX OS Neisseria meningitidis strain EG329.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide

Protein 52..512  
/label= Mature\_NhhA\_deletion\_mutant\_#1  
/note= "Predicted mature protein, specifically  
claimed in claim 12".

MO200155182-A1.  
XX PD 02-AUG-2001.  
XX PF 25-JAN-2001; 2001WO-AU00069.  
XX PR 25-JAN-2000; 2000US-0177917.  
XX PA (UYQU ) UNIV QUEBENSLAND.  
XX PI Peak IRA, Jennings MP;  
XX DR WPI; 2001-488774/53.  
XX DR N-PSDB; AAS09172.  
PT New NhhA surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX Claim 12; Fig 5; 91pp; English.  
XX The present invention relates to the isolation of novel Neisseria  
XX meningitidis mutant polypeptides of the surface antigen NhhA  
XX (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are  
XX characterised by deletions of non-conserved amino acids, particularly  
XX the deletion of variable regions. The deletion mutants are useful in  
XX diagnostics, therapeutic and prophylactic vaccines against a broader  
XX spectrum of N. meningitidis, and in designing and/or screening of  
XX medicaments. The mutant proteins when used as a vaccine can effectively  
XX immunise against a broader spectrum of N. meningitidis strains than  
XX would be expected from a corresponding wild-type surface antigen.  
XX The present sequence represents N. meningitidis strain PMC21 surface  
XX antigen NhhA deletion mutant #1.  
SQ Sequence 512 AA;

Query Match 77.5%; Score 458; DB 22; Length 512;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 TDLTSVGTKEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTLNLT 193  
Db |||||||  
Qy 194 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYTDTVEFLSAD 253  
Db |||||||  
Qy 115 gattnvtndvntddekkraasvkdvl nagwnikvgkpgttasdnvdfvrydtveflsad 174  
Qy 254 TKTTTNNVESKDNKKTEVKIGAKTSVKEKDKGLVTKGKGENGSSTDEGGLVTAKEV 313  
Db |||||||  
Qy 175 tktttnvneskdngkktvkekgaktvikekgdklvtgdkgengsstdegeglvtakev 234  
Qy 314 IDAVNKAQWRMKTNTANGOTGQADKFEVTSCTNVTASGKGTATVSKDDGNTVMD 373  
Db |||||||  
Qy 235 idavnkagwrmtttangtqtgqadkfetvsgntvtfasgkgtatvskddgntvmd 294  
Qy 374 VNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNTIEITRN 433  
Db |||||||  
Qy 295 vnvgdalnvqlnsgwnldskavagssgkvisgnvpskgmdetvnnagntieitrn 354  
Qy 434 GKNIDIATSMPTQSSVSLGAGADAPTLVSVDGDALNVGSKDKNKPVRTITNVAPVKEGDV 493  
Db |||||||  
Qy 355 gknidiatsmtptqfssvslgagadaptilsvdgdalnvsgkdknkpvr itnvpvkegdv 414  
Qy 494 TNVAQLKGVAQLNLRIDNVGNARAGTAQAIATAGLVQAYLPCKSMMAIGGTVRGEAG 553  
Db |||||||  
Qy 415 tnvaqlkgvaqlnlnr idnvgnaragtaqaiataglvqaylpcksmmaiggtvyrgeag 474



CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen NHA deletion mutant #3.  
XX  
SQ Sequence 433 AA;

Query Match 64.5%; Score 381; DB 22; Length 433;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 RAASVKDLNAGWIKGVKPGTASDNVDFVRYDTVEFLSADTKTTNVNVEKDKGKKT 270  
DB |||||||  
53 raasvkdlnagwnlkgvkgpgttasdnvdfvrydtveflsadtktttvnveskngkkt 112  
QY 271 EVKIGAKTSVKEKDKGLVTGKDKGENGSTDEGELVTAKEVIDAVNKAGWRMKTITAN 330  
DB |||||||  
113 evkigaktsvikekgkltvgkdkgensstdegeglvtakevidavnkagwrmtttan 172

QY 331 GGTGADRFETVSGTNVTFASGKGTATVSKDDGDNITVMTDVNVGDALNVQNLQNSGW 390  
DB |||||||  
173 gdtgqadkfetvsgtntvtfasgkgtattvskddgdnitvmtdivnvvgdalnvnqlqnsqw 232

QY 391 NUDSKAVAGSGGKVSIGNVSPSKGMDETVNIAGNNTIETRNKNDIATSMTPQFSV 450  
DB |||||||  
233 nldskavagsgkvsignvspskgmdetvniagnntietrnknidiatsmtpqfssv 292

QY 451 SLGAGADAPTLTSDGDALNVGSKDKNKPVRITNVAPGVKEGDTVNVQALKGVAQLNNRI 510  
DB |||||||  
293 slgagadaptltsvgdalnvgskdknkpvrntnvpagvkegdtnvvaqlkgvaqlnnri 352

QY 511 DNVDGNARAGIAQAATAGLVAQYLPKGSMAIGAIGTTRGEGAGYAIIGYSSISDGNWIIK 570  
DB |||||||  
353 dnvdgnaragiqaataglvaylpkgsmaigagttyrgeagyaigyssisdggnwiiik 412

QY 571 GPASGNSRGHFASASVGVQW 591  
DB |||||||  
413 gtasgnsrghfagasvgyqw 433

RESULT 9  
AAV57045  
ID AAV57045 standard; Protein; 591 AA.  
AC AAV57045;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;  
XX infection; treatment; prevent; antibacterial drug.  
OS *Neisseria meningitidis*.

XX Key Location/Qualifiers  
FH Misc-difference 90  
FT /note= "Encoded by AAT"  
FT Misc-difference 92  
FT /note= "Encoded by GAT"  
FT Misc-difference 98  
FT /note= "Encoded by AAC"  
FT Misc-difference 108  
FT /note= "Encoded by AATC"  
FT Misc-difference 123  
FT /note= "Encoded by ACA"  
FT Misc-difference 269  
FT /note= "Encoded by AAA"  
FT Misc-difference 389

FT /note= "Encoded by CGT"  
XX WO9958683-A2.  
PN  
XX 18-NOV-1999.  
PD  
XX 07-MAY-1999; 99WO-EP03255.  
PF  
XX 13-MAY-1998; 98GB-0010276.  
PR  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA Ruelle J;  
XX  
PI WPI: 2000-053103/04.  
XX N-PSDB; AAZ39865.  
DR  
XX New polypeptide from *neisseria meningitidis* useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC *Haemophilus influenzae* surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with *Neisseria*  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 62.1%; Score 367; DB 21; Length 591;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 124 NFTYSLKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTVHLNGIG 183  
DB |||||||  
124 nftyslkdltdltsvgteklsfsangknvnitsdtkglnfaketagtdtvtvhlngig 183

QY 184 SFLTDTLLNTGATVNTNDNVTDEKKRAASVKDVLNAGWIKGVKPGTASDNVDFVRT 243  
DB |||||||  
184 stltdtllntgattvntndnvtdekkraasvkdvlnagwnikgvkpgttsdnvdfvrt 243

QY 244 YDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGDKGENSGSTDE 303  
DB |||||||  
244 ydtveflsadtktttvnveskdkngkrtevkigaktsvikekdglvtgdkgensgstde 303

QY 304 GEGLVTAKEVIDAVNKAGWRMKTITANGOTGADKFETVTSNTVTFASGKGTATVSKD 363  
DB |||||||  
304 geglvtakevidavnkagwrmtttangotgadkfetvtsntvtfasgkgtattvskd 363

QY 364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVSIGNVSPSKGMDETVNI 423  
DB |||||||  
364 dqgnitvmvdyvngdalnvnqlqnsqwnldskavagssgkvsignvspskgmdetvni 423

QY 424 AGNNTIETRNKNDIATSMTPQFSVSLGACADAPTLSDGDALNVGSKDKNKPVRITN 483  
DB |||||||  
424 agnnietrnknidiatsmtpqfssvslgacadaptlsdgdalnvgskdknkpvrtn 483

QY 484 VAPGVKEDVTNVAQLKGVQAOINLRNIDVGNARAGIAQAIATAGLVQAYLPKSMMAI 543  
 |||||||  
 DB 484 vapgvkedvtnvaqlkgvqaoilnrnidvgnaraglaqataglvqaylpkksmmai 543  
 |||||||  
 QY 544 GGGPYRGEAGYATGYSSISDGGNWIIGKTASGNSRHHFGASASVGYQW 591  
 |||||||  
 DB 544 gggpyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw 591  
 |||||||

RESULT 10  
 AAU06184  
 ID AAU06184 standard; Protein; 407 AA.  
 AC AAU06184;  
 DT 24-OCT-2001 (first entry)  
 DE N. meningitidis PMC21 Nhha deletion mutant #2.  
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
 mutant; mutein.  
 XX Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..51  
 FT /label= Signal\_peptide  
 FT Protein 52..407  
 FT /label= Mature\_Nhha\_deletion\_mutant\_#2  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 XX  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU000069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI; 2001-488774/53.  
 DR N-PSDB; AAS09174.  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 Neisseria meningitidis, useful in producing vaccines for treating or  
 preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 7; 9lpp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 meningitidis mutant polypeptides of the surface antigen Nhha  
 (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 characterized by deletions of non-conserved amino acids, particularly  
 the deletion of variable regions. The deletion mutants are useful in  
 diagnostic, therapeutic and prophylactic vaccines against a broader  
 spectrum of N. meningitidis, and in designing and/or screening of  
 medicaments. The mutant proteins when used as a vaccine can effectively  
 immunise against a broader spectrum of N. meningitidis strains than  
 would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhha deletion mutant #2.  
 XX  
 SQ Sequence 407 AA;

Query Match 60.1%; Score 355; DB 22; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 NVDPVRTYDFVFLSADTKTTTNNVESKDNGKTEVKIGAKTSVIEKDGKLVTKDGKE 296  
 |||||||  
 DB 53 nvdfvrtvdfvflsadtktttvveskdngkktvkvigaktavikekgdklvtkdkge 112  
 |||||||  
 QY 297 NGSSTDEGEGLYTAKEVIDAVNKGWRMKTTTANGOTGOADKEFTVTSCTNTPTFASGKT 356  
 |||||||  
 DB 113 ngstdegegylvakevidavnkgrmktttangqcgadkfetvtsctnvtfasgkt 172  
 |||||||  
 QY 357 TATVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKSKAVAGSSKVIISGNVSPSKGM 416  
 |||||||  
 DB 173 tatvskddqgnitvmydvngdalinvgqlnsgwnldskavagsskvlsngnvspskgm 232  
 |||||||  
 QY 417 DETVINAGNIEITRNGKNIDIAITMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDN 476  
 |||||||  
 DB 233 detvniagnieitrngknidiatsmtqfssvslgagadapltlsvdgdalnvsgkdn 292  
 |||||||  
 QY 477 KPVRIITNVPKGVKEDVTNVAQLKGVQAOINLRNIDVGNARAGIAQAIATAGLVQAYLP 536  
 |||||||  
 DB 293 kpvritnvapgvkedvtnvaqlkgvqaoilnrnidvgnaraglaqataglvqaylp 352  
 |||||||  
 QY 537 GKSMMAIGGTYRGEAGYATGYSSISDGGNWIIGKTASGNSRHHFGASASVGYQW 591  
 |||||||  
 DB 353 gksmmaiggyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw 407  
 |||||||

RESULT 11  
 AAU06186  
 ID AAU06186 standard; Protein; 502 AA.  
 AC AAU06186;  
 DT 24-OCT-2001 (first entry)  
 DE N. meningitidis PMC21 Nhha deletion mutant #4.  
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
 mutant; mutein.  
 XX Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..49  
 FT /label= Signal\_peptide  
 FT Protein 50..502  
 FT /label= Mature\_Nhha\_deletion\_mutant\_#4  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 XX  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU000069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI; 2001-488774/53.  
 DR N-PSDB; AAS09176.  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 Neisseria meningitidis, useful in producing vaccines for treating or  
 preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 9; 9lpp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria



CC The present sequence represents a surface protein of *Neisseria*  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase or antibodies are useful in a kit for  
 CC the detection of diagnosis of *N. meningitidis* infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat *N. meningitidis* infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX  
 SQ Sequence 594 AA;

Query Match 27.2%; Score 161; DB 20; Length 594;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-154;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 GEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFETVTSNVTFAAGKGTATVSKD 363  
 Db 306 geglvtakevidavnkagwrmtttangqtgqadkfetvtsnvtfasgkgtatvskd 365

Qy 364 DOGNITVMYDVMVGNLQNSGNWLDKAVAGSSGKVISGNVSPSKGMDVTNIN 423  
 Db 366 dqgnitvmvdyvgnlqnsqwnldskavagssgkvisgnvpskkgmdetvnin 425

Qy 424 AGNIEITRNGKNIDTSMTPQFSSVSLGAGADAPTLSD 464  
 Db 426 agnieitrngknidiatmtpqfssvslgagadaptlsvd 466

RESULT 14  
 AA157044  
 ID AAY57044 standard; Protein; 594 AA.  
 AC AAY57044;  
 DT 21-FEB-2000 (first entry)  
 DE BASB029 amino acid sequence from *N. meningitidis* strain ATCC13090.  
 KW BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;  
 RW infection; treatment; prevent; antibacterial drug.  
 OS *Neisseria meningitidis*.  
 FH Key Location/Qualifiers  
 FT Misc-difference 104 /note= "Encoded by AATC"  
 FT  
 PN WO9558683-A2.  
 PD 18-NOV-1999.  
 PF 07-MAY-1999; 99WO-EP03255.  
 PR 13-MAY-1998; 98GB-0010276.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Ruelle J;  
 PI  
 DR WPI; 2000-053103/04.  
 DR N-PSDB; AAZ39864.  
 XX New polypeptide from *Neisseria meningitidis* useful for diagnosis,  
 PT treatment or prevention of bacterial infections in mammal -  
 XX  
 PS Claim 4; Fig 2; 74pp; English.  
 XX This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
 CC *Haemophilus influenzae* surface fibril (HSF) protein. The invention  
 CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and

CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
 CC meningitidis infection in a mammal. Compositions containing BASB029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with *Neisseria*  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.

XX  
 SQ Sequence 594 AA;

Query Match 27.2%; Score 161; DB 21; Length 594;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-154;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 GEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFETVTSNVTFAAGKGTATVSKD 363  
 Db 306 geglvtakevidavnkagwrmtttangqtgqadkfetvtsnvtfasgkgtatvskd 365

Qy 364 DOGNITVMYDVMVGNLQNSGNWLDKAVAGSSGKVISGNVSPSKGMDVTNIN 423  
 Db 366 dqgnitvmvdyvgnlqnsqwnldskavagssgkvisgnvpskkgmdetvnin 425

Qy 424 AGNIEITRNGKNIDTSMTPQFSSVSLGAGADAPTLSD 464  
 Db 426 agnieitrngknidiatmtpqfssvslgagadaptlsvd 466

RESULT 15  
 AAU06174  
 ID AAU06174 standard; Protein; 594 AA.  
 AC AAU06174;  
 DT 24-OCT-2001 (first entry)  
 DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.  
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 OS *Neisseria meningitidis* strain EG327.  
 FH Key Location/Qualifiers  
 FT Region 1..50 /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..104 /label= V1  
 FT /note= "Variable region 1"  
 FT 105..116 /label= C2  
 FT /note= "Conserved region 2"  
 FT 117..126 /label= V2  
 FT /note= "Variable region 2"  
 FT 127..190 /label= C3  
 FT /note= "Conserved region 3"  
 FT 191..212 /label= V3  
 FT /note= "Variable region 3"  
 FT 213..231 /label= C4  
 FT /note= "Conserved region 4"





**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 5, 2002, 10:41:15 ; Search time 25.54 Seconds  
(without alignments)  
565.212 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MKKIYRIWNSALNAWAVS.....TASGNSRGHFGASASVGYOW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 2442594 residues

Word size : 20

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	97.0	591	4	US-09-377-155-21
2	573	97.0	591	4	US-09-669-974-21
3	525	88.8	591	4	US-09-377-155-11
4	525	88.8	591	4	US-09-669-974-11
5	432	73.1	592	4	US-09-377-155-2
6	432	73.1	592	4	US-09-669-974-2
7	161	27.2	594	4	US-09-377-155-9
8	161	27.2	594	4	US-09-669-974-9
9	117	19.8	594	4	US-09-377-155-7
10	117	19.8	594	4	US-09-669-974-7
11	117	19.8	598	4	US-09-377-155-13
12	117	19.8	598	4	US-09-669-974-13
13	116	19.6	599	4	US-09-377-155-15
14	116	19.6	599	4	US-09-669-974-15
15	103	17.4	592	4	US-09-377-155-17
16	103	17.4	592	4	US-09-669-974-17
17	93	15.7	589	4	US-09-377-155-19
18	93	15.7	589	4	US-09-669-974-19
19	93	15.7	598	4	US-09-377-155-5
20	93	15.7	598	4	US-09-669-974-5

ALIGNMENTS

RESULT 1  
US-09-377-155-21

; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 97.0%; Score 573; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	VSELTRNHTKRASATVKTAVLATLLFPATVOASANNEEQEEDLYLDPVQRTVAVLIVNSDK	78
DB	19	VSELTRNHTKRASATVKTAVLATLLFPATVOASANNEEQEEDLYLDPVQRTVAVLIVNSDK	78
QY	79	EGTGEKEKVEENSDWAVYNEKGVLTAREITLKAGNLIKQNGTFTYSLKKDLTDLTS	138
DB	79	EGTGEKEKVEENSDWAVYNEKGVLTAREITLKAGNLIKQNGTFTYSLKKDLTDLTS	138
QY	139	VGTEKLSFSANGKNVITSDTKGLNPAKETAGTNGTFTVHLNGIGSTLDTLLNTGATTN	198
DB	139	VGTEKLSFSANGKNVITSDTKGLNPAKETAGTNGTFTVHLNGIGSTLDTLLNTGATTN	198
QY	199	VTNDNVTDDEKKRAASVDVLAAGNLIKGVKPGCTTASDNVDVRYTDTVEFLSADTKTTT	258
DB	199	VTNDNVTDDEKKRAASVDVLAAGNLIKGVKPGCTTASDNVDVRYTDTVEFLSADTKTTT	258
QY	259	VNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKDKGNGSSSTDEGEGLVTAKEVIDAVN	318
DB	259	VNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKDKGNGSSSTDEGEGLVTAKEVIDAVN	318
QY	319	KAGWRMKTTFANGQTQADKFETVTSGTNVTFASGKGTTATVSKDQGNITVMYDVNVGD	378
DB	319	KAGWRMKTTFANGQTQADKFETVTSGTNVTFASGKGTTATVSKDQGNITVMYDVNVGD	378
QY	379	ALNVNQLQNSGHNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKNID	438
DB	379	ALNVNQLQNSGHNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKNID	438
QY	439	IATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTITNVAPGKGDVTNVAQ	498
DB	439	IATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTITNVAPGKGDVTNVAQ	498
QY	499	LKGAQNLRNDNVGDNARAGIAQAIATAGLVQAYLPKSKMMAIGGGYRGGAGYAGY	558
DB	499	LKGAQNLRNDNVGDNARAGIAQAIATAGLVQAYLPKSKMMAIGGGYRGGAGYAGY	558
QY	559	SSISDGGNWIILKGTASGNSRGHFGASASVGYOW	591
DB	559	SSISDGGNWIILKGTASGNSRGHFGASASVGYOW	591

RESULT 2  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 97.0%; Score 573; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 VSELTNRHTKRASATVKTAVLATLLFATVQASANNESQEDLYLDPQRTAVVLVNSDK 78  
DB 19 VSELTNRHTKRASATVKTAVLATLLFATVQASANNESQEDLYLDPQRTAVVLVNSDK 78  
QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFTYSLKKDLTDLTS 138  
DB 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFTYSLKKDLTDLTS 138  
QY 139 VGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTPVHLNGIGSTLTDLTLLNTGATTN 198  
DB 139 VGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTPVHLNGIGSTLTDLTLLNTGATTN 198  
QY 199 VTNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNDVDFVRYTDTVEFLSADTKTTT 258  
DB 199 VTNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNDVDFVRYTDTVEFLSADTKTTT 258  
QY 259 VNVESKDNKGKTEVKIGAKTSVIREKDGKLVTKGDKGKNGSSSTDEGEGLVTAKEVIDAVN 318  
DB 259 VNVESKDNKGKTEVKIGAKTSVIREKDGKLVTKGDKGKNGSSSTDEGEGLVTAKEVIDAVN 318  
QY 319 KAGWRMKTTFANGOTGOADKPFETVTSCTNTVTFASGKGTATVSKDDGNTVMYDYNVGD 378  
DB 319 KAGWRMKTTFANGOTGOADKPFETVTSCTNTVTFASGKGTATVSKDDGNTVMYDYNVGD 378  
QY 379 ALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIEITRNGKNID 438  
DB 379 ALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIEITRNGKNID 438  
QY 439 IATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKPKVRIITNVAPGVKEGDTVNTVAQ 498  
DB 439 IATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKPKVRIITNVAPGVKEGDTVNTVAQ 498  
QY 499 LKGVQALNNRINDVGNARAGIAQATATAGLVQAYLPGKSMMAIGGGTYRGEAGYATGY 558  
DB 499 LKGVQALNNRINDVGNARAGIAQATATAGLVQAYLPGKSMMAIGGGTYRGEAGYATGY 558  
QY 559 SSISDGNWIIKGTASGNSRHFHGASASVGYQW 591  
DB 559 SSISDGNWIIKGTASGNSRHFHGASASVGYQW 591

RESULT 3  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 88.8%; Score 525; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 RTAVVLIVNSDKREGTEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFT 126  
DB 67 RTAVVLIVNSDKREGTEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFT 126  
QY 127 YSLKKDLTDLTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTPVHLNGIGSTL 186  
DB 127 YSLKKDLTDLTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTPVHLNGIGSTL 186  
QY 187 TDTLLNTGATTNTNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNDVDFVRYTDT 246  
DB 187 TDTLLNTGATTNTNDNVTDDEKRAASVKDVLNAGNVIKGVKPGTTASDNDVDFVRYTDT 246  
QY 247 VEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIREKDGKLVTKGDKGKNGSSSTDEGEG 306  
DB 247 VEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIREKDGKLVTKGDKGKNGSSSTDEGEG 306  
QY 307 LVTAKEVIDAVNKAQWRMKTTFANGOTGOADKPFETVTSCTNTVTFASGKGTATVSKDDGQ 366  
DB 307 LVTAKEVIDAVNKAQWRMKTTFANGOTGOADKPFETVTSCTNTVTFASGKGTATVSKDDGQ 366  
QY 367 NITVMYDYNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGN 426  
DB 367 NITVMYDYNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGN 426  
QY 427 NIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKPKVRIITNVAP 486  
DB 427 NIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKPKVRIITNVAP 486  
QY 487 GVKEGDTVNTVAQLKGVQALNNRINDVGNARAGIAQATATAGLVQAYLPGKSMMAIGGG 546  
DB 487 GVKEGDTVNTVAQLKGVQALNNRINDVGNARAGIAQATATAGLVQAYLPGKSMMAIGGG 546  
QY 547 TYRGEAGYATGYSSISDGNWIIKGTASGNSRHFHGASASVGYQW 591  
DB 547 TYRGEAGYATGYSSISDGNWIIKGTASGNSRHFHGASASVGYQW 591

RESULT 4  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 88.8%; Score 525; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTAVAVLIIVNSDKGEGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFT 126  
Db 67 RTAVAVLIIVNSDKGEGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTFT 126

Qy 127 YSLKDLTDLTSVGTGTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186  
Db 127 YSLKDLTDLTSVGTGTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186

Qy 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDT 246  
Db 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDT 246

Qy 247 VEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGSGSSDDEG 306  
Db 247 VEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGSGSSDDEG 306

Qy 307 LVTAKEVIDAVNKAAGWRMKTITANGOTQADKFEFVTSGTNTVFASGKGTATVSKDDQG 366  
Db 307 LVTAKEVIDAVNKAAGWRMKTITANGOTQADKFEFVTSGTNTVFASGKGTATVSKDDQG 366

Qy 367 NITVMYDVGDNALNVQNSGWNLDKAVAGSGKVISGNSVPSKGMDETVNINAGN 426  
Db 367 NITVMYDVGDNALNVQNSGWNLDKAVAGSGKVISGNSVPSKGMDETVNINAGN 426

Qy 427 NIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTINAP 486  
Db 427 NIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTINAP 486

Qy 487 GYKEDGVTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGG 546  
Db 487 GYKEDGVTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGG 546

Qy 547 TYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591  
Db 547 TYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 5  
US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 73.1%; Score 432; DB 4; Length 592;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 59 DLYLDPVQRTVAVLIVNSDKGEGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118  
Db 60 DLYLDPVQRTVAVLIVNSDKGEGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 119

Qy 119 KONGTNFTYSLKKDLTDLTSVGTGTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTTVH 178  
Db 120 KONGTNFTYSLKKDLTDLTSVGTGTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTTVH 179

Qy 179 LNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNV 238  
Db 180 LNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNV 239

Qy 239 DEVRTYDVFELUSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGNG 298  
Db 240 DEVRTYDVFELUSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGNG 299

Qy 299 SSTDEGGLVTAKEVIDAVNKAAGWRMKTITANGOTQADKFEFVTSGTNTVFASGKGT 358  
Db 300 SSTDEGGLVTAKEVIDAVNKAAGWRMKTITANGOTQADKFEFVTSGTNTVFASGKGT 359

Qy 359 TVSKDDQGNITVMYDVGDNALNVQNSGWNLDKAVAGSGKVISGNSVPSKGMDE 418  
Db 360 TVSKDDQGNITVMYDVGDNALNVQNSGWNLDKAVAGSGKVISGNSVPSKGMDE 419

Qy 419 TVNINAGNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKKDNKP 478  
Db 420 TVNINAGNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKKDNKP 479

Qy 479 VRITNVAPCVKEDVTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAYLPCK 538  
Db 480 VRITNVAPCVKEDVTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAYLPCK 539

Qy 539 SMAAGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591  
Db 540 SMAAGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592

RESULT 6  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

```
Query Match      73.1%; Score 432; DB 4; Length 592;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 DLYDDPQVAVLI VNSDKGTGKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118
DB 60 DLYDDPQVAVLI VNSDKGTGKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 119
QY 119 KONGTNTYSLKDLTDLSVGTSEKLSFANGKNVNTSDTKGLNFAKETAAGTNGDTTVH 178
DB 120 KONGTNTYSLKDLTDLSVGTSEKLSFANGKNVNTSDTKGLNFAKETAAGTNGDTTVH 179
QY 179 LINGIGSLTDLTLNTGATTNTNDVTDDEKKRAASVDVNLNAGWNIKVGKPGTTASDNV 238
DB 180 LINGIGSLTDLTLNTGATTNTNDVTDDEKKRAASVDVNLNAGWNIKVGKPGTTASDNV 239
QY 239 DFVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVTKDKGNG 298
DB 240 DFVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVTKDKGNG 299
QY 299 SSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTGA 358
DB 300 SSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTGA 359
QY 359 TVSKDDOGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 418
DB 360 TVSKDDOGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 419
QY 419 TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKP 478
DB 420 TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDNKP 479
QY 479 VRITNAPGVKEGDTNVNVAQLKGAQNLRIDNVNAGNARAGIAQAATAGLVQAYLPCK 538
DB 480 VRITNAPGVKEGDTNVNVAQLKGAQNLRIDNVNAGNARAGIAQAATAGLVQAYLPCK 539
QY 539 SMDAIGCTGREGAGYAGYSSISDGGWNIKGTASGNSRGHFGCASVGYQW 591
DB 540 SMDAIGCTGREGAGYAGYSSISDGGWNIKGTASGNSRGHFGCASVGYQW 592

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/093771155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match      27.2%; Score 161; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.5e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTATVSKD 363
DB 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTATVSKD 365
QY 364 DQGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNI 423
DB 366 DQGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNI 425
QY 424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464
DB 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466

RESULT 9
US-09-377-155-7
; Sequence 7, Application US/093771155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match      27.2%; Score 161; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.5e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTATVSKD 363
DB 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTATVSKD 365
QY 364 DQGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNI 423
DB 366 DQGNITVMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNI 425
QY 424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464
DB 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466

RESULT 9
US-09-377-155-7
; Sequence 7, Application US/093771155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match      27.2%; Score 161; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.5e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFASGKGTATVSKD 363
```



; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 19.6%; Score 116; DB 4; Length 599;  
Best Local Similarity 100.0%; Pred. No. 1.5e-101;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 476 NKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNDRDNDVGNARAGIAQAIAATAGLVQAYL 535  
DB 484 NKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNDRDNDVGNARAGIAQAIAATAGLVQAYL 543  
QY 536 PGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHGFGASASVGYOW 591  
DB 544 PGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHGFGASASVGYOW 599

RESULT 14  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 19.6%; Score 116; DB 4; Length 599;  
Best Local Similarity 100.0%; Pred. No. 1.5e-101;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 476 NKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNDRDNDVGNARAGIAQAIAATAGLVQAYL 535  
DB 484 NKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNDRDNDVGNARAGIAQAIAATAGLVQAYL 543  
QY 536 PGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHGFGASASVGYOW 591  
DB 544 PGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHGFGASASVGYOW 599

RESULT 15  
US-09-377-155-17

; Sequence 17, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-17

Query Match 17.4%; Score 103; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3e-89;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 190 LLNTGATTNVTNDVTDDEKKRAASVKDVLNAGNNIKGVKPGTTASDNDVDFVRYDTYVEF 249  
DB 190 LLNTGATTNVTNDVTDDEKKRAASVKDVLNAGNNIKGVKPGTTASDNDVDFVRYDTYVEF 249  
QY 250 LSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDGKLVTK 292  
DB 250 LSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDGKLVTK 292

Search completed: September 5, 2002, 10:41:17  
Job time: 263 sec





**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:41:54 ; Search time 33.9 Seconds  
(without alignments)  
1675.186 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNMAVVS.....TASGNSRGHFGASASVGQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 20  
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	573	97.0	591	2	G81133
2	137	23.2	592	2	A81888
					adhesin NMB0992 [i probable surface f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TET>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match		97.0%; Score 573; DB 2; Length 591;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 573; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	19	VSELPRNHTKRASATVKTAVLATLLPATVQASANNQEEDLYLDPVQRTVAVLVNSDK 78
Db	19	VSELPRNHTKRASATVKTAVLATLLPATVQASANNQEEDLYLDPVQRTVAVLVNSDK 78
QY	79	EGTGEKEKVEEENSDWAVYENEGVLTAAREITLKAGONLKIQTNGFTYSLKKDLTDLTS 138
Db	79	EGTGEKEKVEEENSDWAVYENEGVLTAAREITLKAGONLKIQTNGFTYSLKKDLTDLTS 138
QY	139	VGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTTHLNGIGSTLTDLTLLTNGATTN 198
Db	139	VGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTTHLNGIGSTLTDLTLLTNGATTN 198
QY	199	VTNDNVTDEKRAASVKDVLNAGWNIKVKPGTTASDNVDFVRYTDTVEFLSADTKTTT 258
Db	199	VTNDNVTDEKRAASVKDVLNAGWNIKVKPGTTASDNVDFVRYTDTVEFLSADTKTTT 258
QY	259	VNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGDKGSGSSDTEGEGLVTAKEVIDAVN 318
Db	259	VNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGDKGSGSSDTEGEGLVTAKEVIDAVN 318
QY	319	KAGWRMKTTTANGQTQADKFEFVTSCTNVTAFASGKGTATVSKDDQGNITVMDYNVGD 378
Db	319	KAGWRMKTTTANGQTQADKFEFVTSCTNVTAFASGKGTATVSKDDQGNITVMDYNVGD 378
QY	379	ALNVNOLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKNID 438
Db	379	ALNVNOLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKNID 438
QY	439	IATSMTPQFSSVSLGAGADAPTLSDGDLNMGSKKDNKPVRTNVPAGVKEGDTNVAQ 498
Db	439	IATSMTPQFSSVSLGAGADAPTLSDGDLNMGSKKDNKPVRTNVPAGVKEGDTNVAQ 498
QY	499	LKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558
Db	499	LKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558
QY	559	SSISDGGNIIKGTASGNSRGHFGASASVGQW 591
Db	559	SSISDGGNIIKGTASGNSRGHFGASASVGQW 591
RESULT 2		
A81888		probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2
C:Species: Neisseria meningitidis		
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001		
C:Accession: A81888		
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo		
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre		
Nature 404, 502-506, 2000		
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491		
A:Reference number: A81775; MUID:20222556		
A:Accession: A81888		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-592 <PAR>		
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737		
A:Experimental source: serogroup A, strain Z2491		
C:Genetics:		
A:Gene: NMA1200		
Query Match		23.2%; Score 137; DB 2; Length 592;
Best Local Similarity		100.0%; Pred. No. 1.8e-131;
Matches 137; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	294	KGENGSTDEGGLVTAKEVIDAVNKGWRMKTNTTANGQTQADKFEFVTSGNVTFTASG 353

Db 294 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFSG 353  
QY 354 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 413  
Db 354 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 413  
QY 414 GKMDETVNINAGNNIEI 430  
Db 414 GKMDETVNINAGNNIEI 430

Search completed: September 5, 2002, 10:41:54  
Job time: 220 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:48:19 ; Search time 19.15 seconds  
(without alignments)  
1194.948 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description
-----	-----	-----

No matches found

Search completed: September 5, 2002, 10:48:19  
Job time: 420 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:47:55 ; Search time 55.95 Seconds  
(without alignments)  
1827.346 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKRIIWNALNAWVVS.....TASGNSRGHGASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 20

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL19.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	573	97.0	591	16 Q9JR18	Q9JR18 neisseria m
2	556	94.1	591	2 Q9JPS7	Q9JPS7 neisseria m
3	525	88.8	591	2 Q93QY3	Q93QY3 neisseria m
4	432	73.1	592	2 Q9AQF0	Q9AQF0 neisseria m
5	220	37.2	526	2 Q9JPS4	Q9JPS4 neisseria m
6	220	37.2	530	2 Q9JPS1	Q9JPS1 neisseria m
7	195	33.0	594	2 Q9JPI3	Q9JPI3 neisseria m
8	195	33.0	594	2 Q9JPS2	Q9JPS2 neisseria m
9	174	29.4	592	2 Q9JPS9	Q9JPS9 neisseria m
10	171	28.9	598	2 Q9JPR7	Q9JPR7 neisseria m
11	171	28.9	599	2 Q9JPS8	Q9JPS8 neisseria m
12	161	27.2	590	2 Q9JPS3	Q9JPS3 neisseria m
13	161	27.2	594	2 Q93QY4	Q93QY4 neisseria m
14	137	23.2	592	16 Q9JQW4	Q9JQW4 neisseria m
15	117	19.8	594	2 Q9JPH7	Q9JPH7 neisseria m
16	117	19.8	598	2 Q9JPR9	Q9JPR9 neisseria m

17 117 19.8 598 2 Q9JPS0 Q9JPS0 neisseria m  
18 116 19.6 599 2 Q9JPR8 Q9JPR8 neisseria m  
19 116 19.6 600 2 Q9JPS6 Q9JPS6 neisseria m  
20 116 19.6 600 2 Q9JPS5 Q9JPS5 neisseria m  
21 103 17.4 592 2 Q93QY2 Q93QY2 neisseria m  
22 93 15.7 589 2 Q9JPI0 Q9JPI0 neisseria m  
23 93 15.7 589 2 Q93QY1 Q93QY1 neisseria m  
24 93 15.7 595 2 Q9JPH0 Q9JPH0 neisseria m  
25 93 15.7 598 2 Q9JPT0 Q9JPT0 neisseria m  
26 93 15.7 598 2 Q93QY5 Q93QY5 neisseria m

#### ALIGNMENTS

RESULT 1  
Q9JR18  
ID Q9JR18 PRELIMINARY; PRT; 591 AA.  
AC Q9JR18;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).  
DE GNA992 OR NMB0992 OR NHHA.  
GN Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491.  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT Meningococcus by Vaccine Candidates Against Serogroup B  
RL Identification of Whole-Genome Sequencing."  
RN [2]  
RC SEQUENCE FROM N.A.  
RP STRAIN=MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizzi M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58".  
RN Science 287:1809-1815(2000).  
RL [3]  
RC SEQUENCE FROM N.A.  
RP SPECIES=N.meningitidis; STRAIN=PMC21;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF226375; AAF42524.1; -  
DR EMBL; AE002450; AAF41395.1; -  
DR EMBL; AF226367; AAF42516.1; -  
DR EMBL; AF226370; AAF42519.1; -  
DR EMBL; AF226374; AAF42523.1; -  
DR EMBL; AF157611; AAK68872.1; -  
DR TIGR; NMB0992; -  
KW Complete proteome.

SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73BC6 CRC64;

Query Match 97.0%; Score 573; DB 16; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEEDLYLDPVQRTVAVLVNSDK 78  
DB 19 VSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEEDLYLDPVQRTVAVLVNSDK 78  
QY 79 EGTCEKEKVEENSDWAVYENKGVLTAREITLKAGDNLIKQNGTFTYSLKDKLDTLTS 138  
DB 79 EGTCEKEKVEENSDWAVYENKGVLTAREITLKAGDNLIKQNGTFTYSLKDKLDTLTS 138  
QY 139 VGTEKLSFSAANGKVNITSQTKGLNFAKETAGTNGDFTVHLNGIGSTLTDLLNTGATN 198  
DB 139 VGTEKLSFSAANGKVNITSQTKGLNFAKETAGTNGDFTVHLNGIGSTLTDLLNTGATN 198  
QY 199 VTNDNVTDDEKRAASVKDVLNAGWNIKGVPKGTASDNVDVFTYDVEFLSADTKTTT 258  
DB 199 VTNDNVTDDEKRAASVKDVLNAGWNIKGVPKGTASDNVDVFTYDVEFLSADTKTTT 258  
QY 259 VNVEKDNKGKTEVKIGAKTSVKEKDKGLVTGKDKGENGSSDDEGEGLVTAKEVIDAVN 318  
DB 259 VNVEKDNKGKTEVKIGAKTSVKEKDKGLVTGKDKGENGSSDDEGEGLVTAKEVIDAVN 318  
QY 319 KAGWRMKTTFANGOTGADKPEVTSGTNTVFASGKGTATVSKDQGNITVMYDYNVGD 378  
DB 319 KAGWRMKTTFANGOTGADKPEVTSGTNTVFASGKGTATVSKDQGNITVMYDYNVGD 378  
QY 379 ALNVNQLONGWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNID 438  
DB 379 ALNVNQLONGWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNID 438  
QY 439 IATSMPTQFSSVSLGADAPTLSDVDGDLNVGSKDKNPVITNVAPGVKEDGVNTVAQ 498  
DB 439 IATSMPTQFSSVSLGADAPTLSDVDGDLNVGSKDKNPVITNVAPGVKEDGVNTVAQ 498  
QY 499 LKGVQALNNRINDVGNARAGIAQATATAGLVQAYLPKGSMAIGGGTYRGEAGYAGY 558  
DB 499 LKGVQALNNRINDVGNARAGIAQATATAGLVQAYLPKGSMAIGGGTYRGEAGYAGY 558  
QY 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
DB 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 2

Q9JPS7 ID Q9JPS7 PRELIMINARY; PRT; 591 AA.  
AC Q9JPS7;  
DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BZ147.  
RA MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,  
RA Galeotti C.D., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1; -  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91ELF CRC64;

Query Match 94.1%; Score 556; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TAVLATLLFATVOASANNEQEEDLYLDPVQRTVAVLVNSDKEGTGEKEKVEEENSDWAV 95  
DB 36 TAVLATLLFATVOASANNEQEEDLYLDPVQRTVAVLVNSDKEGTGEKEKVEEENSDWAV 95  
QY 96 YFNEKGVLTAREITLKAGDNLIKQNGTFTYSLKDKLDTLTSVGTSEKLSFSANGKNVI 155  
DB 96 YFNEKGVLTAREITLKAGDNLIKQNGTFTYSLKDKLDTLTSVGTSEKLSFSANGKNVI 155  
QY 156 TSQTKGLNFAKETAGTNGDFTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKRAASV 215  
DB 156 TSQTKGLNFAKETAGTNGDFTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKRAASV 215  
QY 216 KDVLNAGWNIKGVPKGTASDNVDVFTYDVEFLSADTKTTVNVESKDNKGKTEVKIG 275  
DB 216 KDVLNAGWNIKGVPKGTASDNVDVFTYDVEFLSADTKTTVNVESKDNKGKTEVKIG 275  
QY 276 AKTSVKEKDKGLVTGKDKGENGSSDDEGEGLVTAKEVIDAVNAGWRMKTTFANGOTGO 335  
DB 276 AKTSVKEKDKGLVTGKDKGENGSSDDEGEGLVTAKEVIDAVNAGWRMKTTFANGOTGO 335  
QY 336 ADKFEVTSQNTVFASGKGTATVSKDQGNITVMYDYNVGDALNVNQLONGWNLDSK 395  
DB 336 ADKFEVTSQNTVFASGKGTATVSKDQGNITVMYDYNVGDALNVNQLONGWNLDSK 395  
QY 396 AVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDIASMTQFSSVSLGAG 455  
DB 396 AVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDIASMTQFSSVSLGAG 455  
QY 456 ADAPTLSDVDGDLNVGSKDKNPVITNVAPGVKEDGVNTVAQLKGVQALNNRINDVGN 515  
DB 456 ADAPTLSDVDGDLNVGSKDKNPVITNVAPGVKEDGVNTVAQLKGVQALNNRINDVGN 515  
QY 516 NARAGIAQATATAGLVQAYLPKGSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASG 575  
DB 516 NARAGIAQATATAGLVQAYLPKGSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASG 575  
QY 576 NSRGHFGASASVGYQW 591  
DB 576 NSRGHFGASASVGYQW 591

RESULT 3

Q93QV3 ID Q93QV3 PRELIMINARY; PRT; 591 AA.  
AC Q93QV3;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DE OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157606; AAK68867.1; -  
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;



```
Query Match      88.8%; Score 525; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 RTVAVLVNSDKEGTGEKEKVEENSDWAYFNEKGVLTAREITLKGADNLKIKQNGTNP 126
Db 67 RTVAVLVNSDKEGTGEKEKVEENSDWAYFNEKGVLTAREITLKGADNLKIKQNGTNP 126
QY 127 YSLKKDLTDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
Db 127 YSLKKDLTDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
QY 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNVDFVRTYDT 246
Db 187 TDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNVDFVRTYDT 246
QY 247 VFELSADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDGKLVTKDKGKENGSSSTDEGEG 306
Db 247 VFELSADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDGKLVTKDKGKENGSSSTDEGEG 306
QY 307 LVTAKEVIDAVNKAAGRMMKTTTANGOTGOADKFEFVTSGTNTVTFASGKGTATVSKDDQG 366
Db 307 LVTAKEVIDAVNKAAGRMMKTTTANGOTGOADKFEFVTSGTNTVTFASGKGTATVSKDDQG 366
QY 367 NITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTETVINAGN 426
Db 367 NITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTETVINAGN 426
QY 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAP 486
Db 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAP 486
QY 487 GYKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGRKSMMAIGGG 546
Db 487 GYKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGRKSMMAIGGG 546
QY 547 TYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591
Db 547 TYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 4
Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381BFC5 CRC64;
```

```
Query Match      73.1%; Score 432; DB 2; Length 592;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 DLYLDPVQRTAVLVNSDKETGTEKEKVEENSDWAYFNEKGVLTAREITLKGADNLKI 118
Db 60 DLYLDPVQRTAVLVNSDKETGTEKEKVEENSDWAYFNEKGVLTAREITLKGADNLKI 119
QY 119 KONGTNTYSLKKDLTDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVH 178
```

```
Db 120 KONGTNTYSLKKDLTDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVH 179
QY 179 LNCIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNV 238
Db 180 LNCIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNV 239
QY 239 DFVRTYDTVEFLSADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDGKLVTKDKGKENG 298
Db 240 DFVRTYDTVEFLSADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDGKLVTKDKGKENG 299
QY 299 SSTDSGEGLVTAKEVIDAVNKAAGRMMKTTTANGOTGOADKFEFVTSGTNTVTFASGKGT 358
Db 300 SSTDSGEGLVTAKEVIDAVNKAAGRMMKTTTANGOTGOADKFEFVTSGTNTVTFASGKGT 359
QY 359 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMD 418
Db 360 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMD 419
QY 419 TVNINAGNNIETIRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKP 478
Db 420 TVNINAGNNIETIRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKP 479
QY 479 VRITNVAPGVKSGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGR 538
Db 480 VRITNVAPGVKSGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGR 539
QY 539 SMAAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591
Db 540 SMAAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 592

RESULT 5
Q9JPS4 PRELIMINARY; PRT; 526 AA.
AC Q9JPS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG6/88;
RA MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
  Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226377; AAF42526.1; -.
SQ SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;
```

```
Query Match      37.2%; Score 220; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 YDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTETVINAGNNIET 431
Db 307 YDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTETVINAGNNIET 366
QY 432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVK 491
Db 367 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVK 426
```

```
QY 492 DVTNVAQLKGVAGNLRNIDVDGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYRGE 551
DB 427 DVTNVAQLKGVAGNLRNIDVDGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYRGE 486
QY 552 AGYAIGYSSISDGGNIIKGTASGNSRGHFGCASVGYQW 591
DB 487 AGYAIGYSSISDGGNIIKGTASGNSRGHFGCASVGYQW 526
RESULT 6
Q9JPS1 PRELIMINARY; PRT; 530 AA.
AC Q9JPS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGF26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -.
DR EMBL: AF226369; AAF42518.1; -.
SQ SEQUENCE 530 AA; 55130 MW; 1F836CA57598515B CRC64;

Query Match 37.2%; Score 220; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 YDNNVGDALNVNQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTYNINAGNNIEIT 431
DB 311 YDNNVGDALNVNQLQNSGWNLDKAVAGSGKVISGNVSPSKGMDVTYNINAGNNIEIT 370
QY 432 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKRG 491
DB 371 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKRG 430
QY 492 DVTNVAQLKGVAGNLRNIDVDGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYRGE 551
DB 431 DVTNVAQLKGVAGNLRNIDVDGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYRGE 490
QY 552 AGYAIGYSSISDGGNIIKGTASGNSRGHFGCASVGYQW 591
DB 491 AGYAIGYSSISDGGNIIKGTASGNSRGHFGCASVGYQW 530
RESULT 7
Q9JPT3 PRELIMINARY; PRT; 594 AA.
AC Q9JPT3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, AND BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -.
DR EMBL: AF226369; AAF42518.1; -.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 33.0%; Score 195; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.3e-179;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 KVNITSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDTLLTGATTNTVNDNVTDDEKRR 211
DB 154 KVNITSDTKGLNFAKETAGTNGDITVHLNGIGSTLTDTLLTGATTNTVNDNVTDDEKRR 213
QY 212 AASVKDVLNAGNWKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKE 271
DB 214 AASVKDVLNAGNWKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKE 273
QY 272 VKIGAKTSVLIKEKDGKLVTKGDKGSGSTDEGSLVTAKEVIDAVNKAGRWKTTTANG 331
DB 274 VKIGAKTSVLIKEKDGKLVTKGDKGSGSTDEGSLVTAKEVIDAVNKAGRWKTTTANG 333
QY 332 QTGQADKFEYVTSGT 346
DB 334 QTGQADKFEYVTSGT 348
RESULT 8
Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR EMBL: AF226376; AAF42525.1; -.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F5D3D56 CRC64;

Query Match 33.0%; Score 195; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.3e-179;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 152 KVNITSDFKGLNFAKETAGTNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRR 211
Db 154 KVNITSDFKGLNFAKETAGTNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRR 213
Qy 212 AASVKDVLNAGWNKIGVKPGTASDNVDVFRYDTYDFVFLSADTKTTTNNVESKONGKYTE 271
Db 214 AASVKDVLNAGWNKIGVKPGTASDNVDVFRYDTYDFVFLSADTKTTTNNVESKONGKYTE 273
Qy 272 VKIGAKTSVIEKDGKLVTKGDKGNGSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANG 331
Db 274 VKIGAKTSVIEKDGKLVTKGDKGNGSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANG 333
Qy 332 QTGOADKFEFTVTSGT 346
Db 334 QTGOADKFEFTVTSGT 348
RESULT 9
Q9JPS9 ID Q9JPS9 PRELIMINARY; PRT; 592 AA.
AC Q9JPS9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;
```

```
Query Match 29.4%; Score 174; DB 2; Length 592;
Best Local Similarity 99.6%; Pred. No. 5.9e-159;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 190 LLNTGATTNVTNDVTDDEKRAASVDVLNAGWNKIGVKPGTASDNVDVFRYDTYDFV 249
Db 190 LLNTGATTNVTNDVTDDEKRAASVDVLNAGWNKIGVKPGTASDNVDVFRYDTYDFV 249
Qy 250 LSADTKTTTNNVESKONGKYTEVIGAKTSVIEKDKGLVTGDKGNGSGSTDEGEGLVT 309
Db 250 LSADTKTTTNNVESKONGKYTEVIGAKTSVIEKDKGLVTGDKGNGSGSTDEGEGLVT 309
Qy 310 AKEVIDAVNKGAGWRMKTITANGQTGOADKFEFTVTSGTNVTNVTASGKGTATVSKDDQGNIT 369
Db 310 AKEVIDAVNKGAGWRMKTITANGQTGOADKFEFTVTSGTNVTNVTASGKGTATVSKDDQGNIT 369
Qy 370 VMYDVNVDALNVNOLQNGNLDKAVAGSGKVIISGNVSPSKGKMDETYNINAGNIE 429
Db 370 VMYDVNVDALNVNOLQNGNLDKAVAGSGKVIISGNVSPSKGKMDETYNINAGNIE 429
Qy 430 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTILSD 464
Db 430 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTILSD 464
```

```
RESULT 10
Q9JPR7 ID Q9JPR7 PRELIMINARY; PRT; 598 AA.
AC Q9JPR7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN RP SEQUENCE FROM N.A.
RC STRAIN=SW2107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226385; AAF42534.1; -.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
Query Match 28.9%; Score 171; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.7e-156;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 294 KGENSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANGQTGOADKFEFTVTSGTNVTFASG 353
Db 300 KGENSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANGQTGOADKFEFTVTSGTNVTFASG 359
Qy 354 KGTATVSKDDQGNITVYDVNVDALNVNOLQNGNLDKAVAGSGKVIISGNVSPSK 413
Db 360 KGTATVSKDDQGNITVYDVNVDALNVNOLQNGNLDKAVAGSGKVIISGNVSPSK 419
Qy 414 GKMDETYNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTILSD 464
Db 420 GKMDETYNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTILSD 470
RESULT 11
Q9JPS8 ID Q9JPS8 PRELIMINARY; PRT; 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
```

AC Q93QY4;  
DT 01-DEC-2001 (TFMBl:rel 19 Created)

RT Meningococcus by Whole-Genome Sequencing.":

RL Science 287:1816-1820(2000).  
DR EMBL; AL162755; CAB84461.1; -  
DR EMBL; AF226357; AAF42506.1; -  
DR EMBL; AF226365; AAF42514.1; -  
DR EMBL; AF226373; AAF42522.1; -  
DR EMBL; AF226386; AAF42535.1; -  
KW Complete proteome.  
SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Search completed: September 5, 2002, 10:47:57  
Job time: 428 sec

Query Match 23.2%; Score 137; DB 16; Length 592;  
Best Local Similarity 100.0%; Pred. No. 2.9e-123;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KGENSSSTDEGELVTAKEVIDAVNKGWRMKTTTANGOTGOADKFETVTSCTNVTFSAG 353  
|||||  
DB 294 KGENSSSTDEGELVTAKEVIDAVNKGWRMKTTTANGOTGOADKFETVTSCTNVTFSAG 353  
|||||  
QY 354 KCTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSK 413  
|||||  
DB 354 KCTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSK 413  
|||||  
QY 414 GKMDETVINAGNNIEI 430  
|||||  
DB 414 GKMDETVINAGNNIEI 430  
|||||

RESULT 15  
Q9JPH7 PRELIMINARY; PRT; 594 AA.  
AC Q9JPH7;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198, AND 297-0;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Conanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF226368; AAF42517.1; -  
DR EMBL; AF226358; AAF42507.1; -  
DR EMBL; AF157604; AAK6865.1; -  
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 19.8%; Score 117; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 5.8e-104;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPKGTAS 235  
|||||

Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPKGTAS 237  
QY 236 DNVDFVRTYDIVERLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292  
|||||  
Db 238 DNVDFVRTYDIVERLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 294  
|||||

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:33:13 ; Search time 58.74 Seconds  
(without alignments)  
1123.218 Million cell updates/sec

Title: US-09-700-293-2

Perfect score: 594

Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 20

Total number of hits satisfying chosen parameters: 39

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_032802.\*

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	100.0	594	AAV23740	A surface protein
2	594	100.0	594	AAV57044	BASH029 amino acid
3	594	100.0	594	AAU06174	N. meningitidis EG
4	161	27.1	407	AAU06184	N. meningitidis PM
5	161	27.1	433	AAU06185	N. meningitidis PM
6	161	27.1	502	AAU06186	N. meningitidis PM
7	161	27.1	512	AAU06182	N. meningitidis PM
8	161	27.1	591	AAV27202	Amino acid sequenc
9	161	27.1	591	AAV23741	A surface protein
10	161	27.1	591	AAV23746	A surface protein
11	161	27.1	591	AAV57045	BASH029 amino acid

12	161	27.1	591	22	AAU06171	N. meningitidis PM
13	161	27.1	591	22	AAU06175	N. meningitidis EG
14	161	27.1	592	20	AAV23737	A surface protein
15	138	23.2	513	22	AAU06183	N. meningitidis H4
16	138	23.2	589	20	AAV23745	A surface protein
17	138	23.2	589	22	AAU06173	N. meningitidis P2
18	138	23.2	592	20	AAV23744	A surface protein
19	138	23.2	592	22	AAU06172	N. meningitidis H4
20	138	23.2	598	20	AAV23738	A surface protein
21	138	23.2	598	20	AAV23742	A surface protein
22	138	23.2	598	22	AAU06177	N. meningitidis H1
23	138	23.2	598	22	AAU06178	N. meningitidis B2
24	127	21.4	592	20	AAU27203	Amino acid sequenc
25	127	21.4	592	22	AAU06180	N. meningitidis Z2
26	98	16.5	245	20	AAV27201	Amino acid sequenc
27	94	15.8	599	20	AAV23743	A surface protein
28	94	15.8	599	22	AAU06176	N. meningitidis H3
29	93	15.7	594	20	AAV23739	A surface protein
30	93	15.7	594	22	AAU06179	N. meningitidis B2
31	82	13.8	116	21	AAV37832	Neisserial conserv
32	72	12.1	72	21	AAV37830	Neisserial conserv
33	59	9.9	604	22	AAU06181	N. meningitidis su
34	43	7.2	53	21	AAV37828	Neisserial conserv
35	32	5.4	56	21	AAV37827	Neisserial conserv
36	23	3.9	1098	17	AAV99392	Haemophilus adhesi
37	22	3.7	2353	17	AAV99393	Haemophilus influe
38	22	3.7	2411	21	AAV23860	Neisserial conserv
39	20	3.4	20	21	AAV37831	Neisserial conserv

#### ALIGNMENTS

RESULT 1  
AAV23740  
ID AAV23740 standard; Protein; 594 AA.  
XX AAV23740:  
XX  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
SW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
XX Neisseria meningitidis.  
OS  
XX WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
XX N-PSDB; AAX85792.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX  
PS Claim 1; Page 100-101; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;

Query Match 100.0%; Score 594; DB 20; Length 594;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATATLLFATVQASTDDDDLYLE 60  
Db 1 mnkiyriiwnlsalnawvavseltrnhtkrasatvatatllfatvqastdddddlyle 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdkegtgekevtedsnwgyfdkkgvltagtitlkagdnlikikqntne 120  
QY 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKKTATNGDITVH 180  
Db 121 ntnassftyssllkdltdltsvgtseklfsfnsankvnitsdtkglnfakktatngdttvh 180  
QY 181 LNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGVKPGTASDNV 240  
Db 181 lngigstldtllntgattnvtndvtddekraasvkdvlagnwnigvkgpgttasdnv 240  
QY 241 DFVRTYDTVEFLSADTKTTTNAVSKDNGKRTVTKIGAKTSVTKEDGKLVTGDKDGEN 300  
Db 241 dfvrtvdtveflsadtktttnavskdngkrtevkigaktsvtekdgklvtgdkdgen 300  
QY 301 SSTDKGEGLYTAKEVIDAVNKGWRMKTITANGOTQADKFEVTSGTNVTFAASKGTTA 360  
Db 301 sstdkgeglvtakevidavnkgwrmtttangotqadkfetvtsgtntvtfasgkgtta 360  
QY 361 TVSKDDGNTITVMYDVNVGDALNVNQLSGWNLDKAVAGSSGKVISGNSVPSGKMD 420  
Db 361 tvskddgntitvmvdydvngdnlvvnqlsgwnldskavagssgkvisgnspsgkmd 420  
QY 421 TVNINAGNNEITRNKNDIATSMTPQFSSVSGACADAPTLSVDDEGALNVGSKDANK 480  
Db 421 tvninagnneitrnknkndiatmtpfssvsgacadaptlsvdddegalnvgskdank 480  
QY 481 PVRLTNVAPGVKEGDTNVAOLKGYAONLNHIDNVGNARAGIAQATATAGLYOAYLPG 540  
Db 481 pvrlnvapgvekdtnvaolkgyaonlnhndvngnaragiaqatataaglyoaylpg 540  
QY 541 KSMWAGGTYRGEAGYAGTSSISDGNWIIKGTASGNSRGHFGASASVGVQW 594  
Db 541 ksmwaggytyrgeagyaigtssisdgnwiikgtasgnsrghfgasasvgyqw 594

RESULT 2

AA57044  
ID AA57044 standard; Protein; 594 AA.

XX AC AA57044;

XX DT 21-FEB-2000 (first entry)

XX DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

XX KW BASB029; *Neisseria meningitidis*; surface fibrin protein; HSF; diagnosis;  
XX infection; treatment; prevent; antibacterial drug.

XX OS *Neisseria meningitidis*.

XX Key Location/Qualifiers

XX FT Misc-difference 104

XX FT /note= "Encoded by AATC"

PN WO9958683-A2.  
XX 18-NOV-1999.  
XX PF 07-MAY-1999; 99WO-EP03255.  
XX PR 13-MAY-1998; 98GB-0010276.  
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Ruelle J;  
XX WPI: 2000-053103/04.  
XX N-PSDB; AA239864.  
XX New polypeptide from *Neisseria meningitidis* useful for diagnosis,  
XX treatment or prevention of bacterial infections in mammals -  
XX Claim 4; Fig 2; 74pp; English.  
XX This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
XX serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
XX Haemophilus influenzae surface fibrin (HSF) protein. The invention  
XX relates to BASB029 polynucleotide sequences (AA239864-239865) and  
XX polypeptide sequences (AA239864-239865) and their immunogenic fragments.  
XX BASB029 polypeptides are useful in a method of diagnosing *Neisseria*  
XX meningitidis infection in a mammal. Compositions containing BASB029  
XX polynucleotides and polypeptides are useful for generating an immune  
XX response in an animal. A therapeutic composition comprising an antibody  
XX directed against BASB029 is useful in treating humans with *Neisseria*  
XX meningitidis disease. The polynucleotide is useful in the diagnosis of  
XX the stage of infection, type of infection, susceptibility to an  
XX infection which results from increased or decreased expression of the  
XX polynucleotide, and for therapeutic or prophylactic purposes.  
XX particularly genetic immunisation. Antibodies against BASB029  
XX polynucleotides and polypeptides are also useful for treating infections  
XX particularly bacterial infections. The protein is useful in the  
XX screening and development of antibacterial drugs. Fused recombinant  
XX protein is useful for the stimulation of the immune system of an organism  
XX receiving the protein.  
XX Sequence 594 AA;

Query Match 100.0%; Score 594; DB 21; Length 594;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATATLLFATVQASTDDDDLYLE 60  
Db 1 mnkiyriiwnlsalnawvavseltrnhtkrasatvatatllfatvqastdddddlyle 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdkegtgekevtedsnwgyfdkkgvltagtitlkagdnlikikqntne 120  
QY 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNFAKKTATNGDITVH 180  
Db 121 ntnassftyssllkdltdltsvgtseklfsfnsankvnitsdtkglnfakktatngdttvh 180  
QY 181 LNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGVKPGTASDNV 240  
Db 181 lngigstldtllntgattnvtndvtddekraasvkdvlagnwnigvkgpgttasdnv 240  
QY 241 DFVRTYDTVEFLSADTKTTTNAVSKDNGKRTVTKIGAKTSVTKEDGKLVTGDKDGEN 300  
Db 241 dfvrtvdtveflsadtktttnavskdngkrtevkigaktsvtekdgklvtgdkdgen 300  
QY 301 SSTDKGEGLYTAKEVIDAVNKGWRMKTITANGOTQADKFEVTSGTNVTFAASKGTTA 360  
Db 301 sstdkgeglvtakevidavnkgwrmtttangotqadkfetvtsgtntvtfasgkgtta 360  
QY 361 TVSKDDGNTITVMYDVNVGDALNVNQLSGWNLDKAVAGSSGKVISGNSVPSGKMD 420  
Db 361 tvskddgntitvmvdydvngdnlvvnqlsgwnldskavagssgkvisgnspsgkmd 420



```
|||||
Db 361 tvskddggnievmvdydnvvgdalinvnqlnsgwnldskavagssgkvvisgnvpskgnknde 420
Qy 421 TVNINAGNNIEITRNKKNIDTATSWTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 480
Db 421 tvninagnnieitrngknidatstmpqfssvslgagadaptslvdddegainvsgskdank 480
Qy 481 PVRITNAPGVKEGSDVTNVAQLKGVAQNLNNHIDNVDCGNARAGIAQAIAATAGLVQAYLPG 540
Db 481 pvrnitnvpagvkegdvtnvqkqvagnlnnhidnvdgnaragiaqaiataglvqaylpg 540
Qy 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
Db 541 ksmaiaigggttyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 3
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX AC
XX AC AAU06174;
XX DT
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain EG327.
XX FH
XX FH Key Location/Qualifiers
XX FT Region 1..50
XX FT /label= C1
XX FT /note= "Conserved region 1"
XX FT Region 51..104
XX FT /label= V1
XX FT /note= "Variable region 1"
XX FT Region 105..116
XX FT /label= C2
XX FT /note= "Conserved region 2"
XX FT Region 117..126
XX FT /label= V2
XX FT /note= "Variable region 2"
XX FT Region 127..190
XX FT /label= C3
XX FT /note= "Conserved region 3"
XX FT Region 191..212
XX FT /label= V3
XX FT /note= "Variable region 3"
XX FT Region 213..231
XX FT /label= C4
XX FT /note= "Conserved region 4"
XX FT Region 232..238
XX FT /label= V4
XX FT /note= "Variable region 4"
XX FT Region 239..594
XX FT /label= C5
XX FT /note= "Conserved region 5"
XX PN
XX PN WO200155182-A1.
XX PD
XX PD 02-AUG-2001.
XX PF
XX PF 25-JAN-2001; 2001WO-AU00069.
XX PR
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09164.
DR
```

```
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis; useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 9lpp; English.
PS
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX SQ Sequence 594 AA;
XX Query Match 100.0%; Score 594; DB 22; Length 594;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQAATDDDDLYLE 60
Db 1 mnkiyriiwsalnawavseltrnhtkrasatvataavlattllfatvgastddddlyle 60
Qy 61 PVORTAVLSRSDKEGTECEKTEVDSNWGVYDFKGLVLTAGTITLKAGDNLKIKONTNE 120
Db 61 pvqrtavvlsrfsrskdtegektevdsnwgvdfdkglvltagtitlkagdnlikqntne 120
Qy 121 NTNASSFTYSLKKDLTDLTSGTEKLSFSAANSKNVNIITSDTKLNFPAKTAETNGDTTVH 180
Db 121 ntnassfty slkddltldtsgteklslfsaansknvnitsdtkglnfaktaetngdttvh 180
Qy 181 LNGIGSTLTDLTLLNGATTNVTNDVDEKKRAASVKDVLNAGWNIKGVKPGTASDNV 240
Db 181 lngigstltdltllntgattntvndvdekkraasvkdvlnagwnikgvkpgttasdnv 240
Qy 241 DVRTYDTVEFLSADTKTTNVNVEKDKRTEVKIGAKTSVIEKDGKLVTKDKGEND 300
Db 241 dfvrtvdtveflsadtkttvnveskdngkrtevkigaktsviekdgklvtgdkgend 300
Qy 301 SSTDKGEGLVTAKEVIDAVNKAQWIKMTTANGQTQADKFPETVTSCTNVTFAKSGGTGA 360
Db 301 sstdkgeglvtakevidavnkagwmkmttangqtqadkfpetvtsctnvtfasggtga 360
Qy 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLSKAVAGSSGKVISGNVSPSKGKMD 420
Db 361 tvskddqgnitvmvdydnvvgdalinvnqlnsgwnldskavagssgkvvisgnvpskgnknde 420
Qy 421 TVNINAGNNIEITRNKKNIDTATSWTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 480
Db 421 tvninagnnieitrngknidatstmpqfssvslgagadaptslvdddegainvsgskdank 480
Qy 481 PVRITNAPGVKEGSDVTNVAQLKGVAQNLNNHIDNVDCGNARAGIAQAIAATAGLVQAYLPG 540
Db 481 pvrnitnvpagvkegdvtnvqkqvagnlnnhidnvdgnaragiaqaiataglvqaylpg 540
Qy 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
Db 541 ksmaiaigggttyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 4
AAU06184
ID AAU06184 standard; Protein; 407 AA.
```

```
XX AC AAU06184;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 Nhha deletion mutant #2.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
XX KW mutant; mutain.
XX OS Neisseria meningitidis strain PMC21.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..51
XX FT Protein /label= Signal_peptide
XX FT 52..407
XX FT /label= Mature_Nhha_deletion_mutant_#2
XX FT /note= "Predicted mature protein, specifically
XX FT claimed in claim 12"
XX PN WO200155182-A1.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU000069.
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX DR WPI: 2001-488774/53.
XX DR N-PSDB; AAS09174.
XX XX
XX PT New Nhha surface antigen polypeptides and polynucleotides from
XX PT Neisseria meningitidis, useful in producing vaccines for treating or
XX PT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 12; Fig 7; 91pp; English.
XX XX
XX CC The present invention relates to the isolation of novel Neisseria
XX CC meningitidis mutant polypeptides of the surface antigen Nhha
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX CC characterised by deletions of non-conserved amino acids, particularly
XX CC the deletion of variable regions. The deletion mutants are useful in
XX CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX CC spectrum of N. meningitidis, and in designing and/or screening of
XX CC medicaments. The mutant proteins when used as a vaccine can effectively
XX CC immunise against a broader spectrum of N. meningitidis strains than
XX CC would be expected from a corresponding wild-type surface antigen.
XX CC The present sequence represents N. meningitidis strain PMC21 surface
XX CC antigen Nhha deletion mutant #2.
XX SQ Sequence 407 AA;

Query Match 27.1%; Score 161; DB 22; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.le-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSCTNVTTFASGKGTATVSKD 365
Db 120 geglvtakevidavnnkagwrmtkttangqtgqadkfetvtsctnvttfasgkgtatvskd 179
QY 366 DQGNITVMDYDVGDALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDEVTNIN 425
Db 180 dqnitvmydvnvgdalinqlngswnlndskavagssgkvisgnvpskgkmdetvnn 239
QY 426 AGNNIEITRNGKNIDIAFMTPTQPSVSLGAGADAPTLSVD 466
Db 240 agnnieitrngknidiatsmtptqfssvslgagadaptilsvd 280
```

```
RESULT 5
AAU06185
ID AAU06185 standard; Protein; 433 AA.
XX AC AAU06185;
XX XX
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 Nhha deletion mutant #3.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
XX KW mutant; mutain.
XX OS Neisseria meningitidis strain PMC21.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..51
XX FT Protein /label= Signal_peptide
XX FT 52..433
XX FT /label= Mature_Nhha_deletion_mutant_#3
XX FT /note= "Predicted mature protein, specifically
XX FT claimed in claim 12"
XX PN WO200155182-A1.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU000069.
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX DR WPI: 2001-488774/53.
XX DR N-PSDB; AAS09175.
XX XX
XX PT New Nhha surface antigen polypeptides and polynucleotides from
XX PT Neisseria meningitidis, useful in producing vaccines for treating or
XX PT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 12; Fig 8; 91pp; English.
XX XX
XX CC The present invention relates to the isolation of novel Neisseria
XX CC meningitidis mutant polypeptides of the surface antigen Nhha
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX CC characterised by deletions of non-conserved amino acids, particularly
XX CC the deletion of variable regions. The deletion mutants are useful in
XX CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX CC spectrum of N. meningitidis, and in designing and/or screening of
XX CC medicaments. The mutant proteins when used as a vaccine can effectively
XX CC immunise against a broader spectrum of N. meningitidis strains than
XX CC would be expected from a corresponding wild-type surface antigen.
XX CC The present sequence represents N. meningitidis strain PMC21 surface
XX CC antigen Nhha deletion mutant #3.
XX SQ Sequence 433 AA;

Query Match 27.1%; Score 161; DB 22; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.le-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSCTNVTTFASGKGTATVSKD 365
Db 146 geglvtakevidavnnkagwrmtkttangqtgqadkfetvtsctnvttfasgkgtatvskd 205
QY 366 DQGNITVMDYDVGDALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDEVTNIN 425
Db 146 dqnitvmydvnvgdalinqlngswnlndskavagssgkvisgnvpskgkmdetvnn 425
```

Db 206 dqgnitvmydvngdlnvnglqnswnldskavagsgkvisgnvpskgkmdetvnnin 265  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466  
|||||  
Db 266 agnieitrngknidiatsmtpqfssvslgagadaptilsvd 306  
RESULT 6  
AAU06186  
ID AAU06186 standard; Protein; 502 AA.  
XX AAU06186;  
AC  
XX 24-OCT-2001 (first entry)  
DT  
XX N. meningitidis PMC21 Nhha deletion mutant #4.  
DE  
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; muteln.  
KW  
XX Neisseria meningitidis strain PMC21.  
OS  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..49  
FT /label= Signal\_peptide  
FT Protein 50..502  
FT /label= Mature\_Nhha\_deletion\_mutant\_#4  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12".  
XX  
XX WO200155182-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
XX  
XX WPI; 2001-488774/53.  
XX  
XX N-PSDB; AAS09176.  
XX  
XX New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
XX Claim 12; Fig 9; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhha deletion mutant #4.  
XX  
XX Sequence 502 AA;  
SQ  
Query Match 27.1%; Score 161; DB 22; Length 502;  
Best Local Similarity 100.0%; Pred. NO. 1.3e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSNTVTFASGKGTTATVSKD 365

Db 215 geglvtakevidavnkagwrmtttangqtgqadkfetvtsntvtfasgkgttatvskd 274  
QY 366 DOGNITVMYDVNGDALNVNQLNSWNLDSKAVAGSGKVISGNVPSKGKMDETVNNIN 425  
|||||  
Db 275 dqgnitvmydvngdlnvnglqnswnldskavagsgkvisgnvpskgkmdetvnnin 334  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466  
|||||  
Db 335 agnieitrngknidiatsmtpqfssvslgagadaptilsvd 375  
RESULT 7  
AAU06182  
ID AAU06182 standard; Protein; 512 AA.  
XX  
AC AAU06182;  
XX 24-OCT-2001 (first entry)  
DT  
XX N. meningitidis PMC21 Nhha deletion mutant #1.  
DE  
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; muteln.  
KW  
XX Neisseria meningitidis strain PMC21.  
OS  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide  
FT Protein 52..512  
FT /label= Mature\_Nhha\_deletion\_mutant\_#1  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12".  
XX  
XX WO200155182-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
XX  
XX WPI; 2001-488774/53.  
XX  
XX N-PSDB; AAS09172.  
XX  
XX New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
XX Claim 12; Fig 5; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhha deletion mutant #1.  
XX  
XX Sequence 512 AA;  
SQ

Query Match 27.1%; Score 161; DB 22; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-149; Indels 0; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVNSKD 365  
 DB 225 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVNSKD 284  
 QY 366 DQGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 425  
 DB 285 DQGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 344  
 QY 426 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 466  
 DB 345 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 385

RESULT 8  
 AAY27202  
 ID AAY27202 standard; Protein; 591 AA.  
 AC AAY27202;  
 XX  
 DT 24-SEP-1999 (first entry)  
 XX  
 DE Amino acid sequence of N. meningitidis protein ORF40-1.  
 XX  
 KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
 KW bacterial infection; treatment.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO9936544-A2.  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 14-JAN-1999; 99WO-IB00103.  
 XX  
 PR 09-OCT-1998; 98GB-0022143.  
 PR 14-JAN-1998; 98GB-0000760.  
 PR 01-SEP-1998; 98GB-0019015.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 XX  
 PI Grandi G, Massignani V, Pizza M, Rappuoli R, Scarlato V;  
 XX  
 XX WPI: 1999-444400/37.  
 DR N-PSDB; AAX99124.  
 XX  
 XX New protein and its nucleotide sequence, useful in vaccines or  
 PT diagnostic compositions for treating and/or preventing Neisseria  
 XX meningitidis infections  
 XX  
 PS Claim 1; Page 62; 123pp; English.  
 XX  
 CC The invention provides proteins (AAY27201-245) from Neisseria  
 CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
 CC encoding the proteins. Compositions comprising the protein, nucleic acid  
 CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
 CC vaccine composition or a diagnostic composition. The composition is also  
 CC useful for treating or preventing an infection due to Neisseria  
 CC bacteria, especially Neisseria meningitidis.  
 XX  
 SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVNSKD 365  
 DB 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVNSKD 363

QY 366 DQGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 425  
 DB 364 DQGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 423  
 QY 426 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 466  
 DB 424 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 464

RESULT 9  
 AAY23741  
 ID AAY23741 standard; Protein; 591 AA.  
 XX  
 AC AAY23741;  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 DE A surface protein of Neisseria meningitidis.  
 XX  
 KW Surface protein; surface glycoprotein; infection; vaccine;  
 KW immunoreactive peptide.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO9931132-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-AU01031.  
 XX  
 PR 12-DEC-1997; 97GB-0026398.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYOU) UNIV QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA;  
 XX  
 DR WPI: 1999-418754/35.  
 DR N-PSDB; AAX85793.  
 XX  
 XX Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 104-106; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 XX  
 SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVNSKD 365  
 DB 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSCTNVTTFASGKGTATVNSKD 363  
 QY 366 DQGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 425  
 DB 364 DQGNITVMDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNNIN 423  
 QY 426 AGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDV 466

Db 424 agnnieitrngkniatstmpqfssvslgagadaptilsvd 464

## RESULT 10

RAY23746  
ID AAY23746 standard; Protein; 591 AA.

XX AC AAY23746;  
XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;  
XX KW immunoreactive peptide.  
XX OS Neisseria meningitidis.

XX PN WO9931132-A1.  
XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.  
XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.  
XX PA (UYQU ) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX DR WPI; 1999-418754/35.  
XX DR N-PSDB; AAX85798.

XX PT Neisseria meningitidis surface proteins useful for treating N.  
XX PT meningitidis infections

XX PS Claim 1; Page 127-128; 132pp; English.

XX CC The present sequence represents a surface protein of Neisseria  
XX CC meningitidis which is approximately 62 kDa. The N. meningitidis  
XX CC surface glycoproteins, nucleic acids, the primers and optionally  
XX CC a thermostable polymerase, or antibodies are useful in a kit for  
XX CC the detection or diagnosis of N. meningitidis infection in humans.  
XX CC The N. meningitidis surface glycoproteins can also be used to  
XX CC prevent or treat N. meningitidis infection in humans, especially  
XX CC in the form of vaccines. The proteins and antibodies can also  
XX CC be used to identify immunoreactive peptides.

XX SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 306 GEGLVTAKEVIDAVNKAGWRMKTTFANGOTGQADKFETVTGNTVTFASGKGTATVSKD 365

|||||  
Db 304 geglvtakevldavnkagwrmtttangtqgqadkfetvtgntvtfasgkgtatvskd 363

|||||  
Oy 366 DOGNTITVMYDVGDNALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDFTVNIN 425

|||||  
Db 364 dqgnitvmydvngdnlvngqlqnsqwnldskavagsgkvisgnvpskqkmdetvnn 423

Oy 426 AGNNIEITRNGKNIIDIAISWTPQFSSVSLGAGADAPTILSD 466

|||||  
Db 424 agnnieitrngkniatstmpqfssvslgagadaptilsvd 464

## RESULT 11

RAY57045

ID AAY57045 standard; Protein; 591 AA.

XX

AC AAY57045;

XX DT 21-FEB-2000 (first entry)

XX DE BASB029 amino acid sequence from N. meningitidis strain H44/76.

XX KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnostics;  
XX KW infection; treatment; prevent; antibacterial drug.

XX OS Neisseria meningitidis.

XX FH Key Location/Qualifiers

FT Misc-difference 90 /note= "Encoded by AAT"

FT Misc-difference 92 /note= "Encoded by GAT"

FT Misc-difference 98 /note= "Encoded by AAC"

FT Misc-difference 108 /note= "Encoded by AATC"

FT Misc-difference 123 /note= "Encoded by ACA"

FT Misc-difference 269 /note= "Encoded by AAA"

FT Misc-difference 389 /note= "Encoded by CGT"

XX PN WO9958683-A2.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-EP03255.

XX PR 13-MAY-1998; 98GB-0010276.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Ruelle J;

XX DR WPI; 2000-053103/04.

XX DR N-PSDB; AAZ39865.

XX CC New polypeptide from neisseria meningitidis useful for diagnosis,  
XX CC treatment or prevention of bacterial infections in mammal

XX PS Claim 4; Fig 2; 74pp; English.

XX CC This is the Neisseria meningitidis BASB029 amino acid sequence from  
XX CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
XX CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
XX CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
XX CC polypeptide sequences (AAY57044-57045) and their immunogenic fragments.  
XX CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
XX CC meningitidis infection in a mammal. Compositions containing BASB029  
XX CC polynucleotides and polypeptides are useful for generating an immune  
XX CC response in an animal. A therapeutic composition comprising an antibody  
XX CC directed against BASB029 is useful in treating humans with Neisseria  
XX CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
XX CC the stage of infection, type of infection, susceptibility to an  
XX CC infection which results from increased or decreased expression of the  
XX CC polynucleotide, and for therapeutic or prophylactic purposes,  
XX CC particularly genetic immunisation. Antibodies against BASB029  
XX CC polynucleotides and polypeptides are also useful for treating infections  
XX CC particularly bacterial infections. The protein is useful in the  
XX CC screening and development of antibacterial drugs. Fused recombinant  
XX CC protein is useful for the stimulation of the immune system of an organism  
XX CC receiving the protein.

XX SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 21; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 306 GEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEFTVSGTNTVFASGKGTATVSKD 365
DB 304 geglvtakevldavnkagwrmtktitangtqgdkfetvsgtntvfaskgttatvskd 363
QY 366 DQGNITVMYDVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425
DB 364 dognitvmymvgdalinvnqlnsgwnldskavagsgkvvisgnvpsksgkmdetvnin 423
QY 426 AGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVD 466
DB 424 agnnieitrngknidatstmpqfssvslgagadaptslsvd 464
```

## RESULT 12

AAU06171 ID AAU06171 standard; Protein; 591 AA.

AC AAU06171;

XX 24-OCT-2001 (first entry)

DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

OS Neisseria meningitidis strain PMC21.

XX

XX Key Location/Qualifiers

FT Peptide 1..51

FT Region 1..50 /label= Signal\_peptide

FT Region 1..50 /label= C1

FT Region 51..108 /note= "Conserved region 1"

FT Region 51..108 /label= V1

FT Protein 52..591

FT /label= Mature\_Nhha

FT /note= "Predicted mature protein, specifically

FT Region 109..120

FT /label= C2

FT Region 121..124 /note= "Conserved region 2"

FT Region 125..188 /label= V2

FT Region 189..210 /note= "Variable region 2"

FT Region 211..229 /label= C3

FT Region 230..236 /label= V3

FT Region 237..259 /note= "Variable region 3"

FT Region 280..286 /label= C4

FT Region 290..296 /label= V4

FT Region 327..391 /note= "Variable region 4"

FT Region 423..491 /label= C5

FT Region 523..591 /note= "Conserved region 5"

XX WO200155182-A1.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

PR (UYOU ) UNIV QUEENSLAND.

PA

XX Peak IRA, Jennings MP;

PI WPI; 2001-488774/53.

DR N-PSDB; AAS09161.

XX New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

XX Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild-type surface antigen Nhha

CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

XX the present invention.

XX Sequence 591 AA;

Query Match 27.1%; Score 161; DB 22; Length 591;

Best Local Similarity 100.0%; Pred. NO. 1.5e-149;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEFTVSGTNTVFASGKGTATVSKD 365

DB 304 geglvtakevldavnkagwrmtktitangtqgdkfetvsgtntvfaskgttatvskd 363

QY 366 DQGNITVMYDVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425

DB 364 dognitvmymvgdalinvnqlnsgwnldskavagsgkvvisgnvpsksgkmdetvnin 423

QY 426 AGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVD 466

DB 424 agnnieitrngknidatstmpqfssvslgagadaptslsvd 464

## RESULT 13

AAU06175 ID AAU06175 standard; Protein; 591 AA.

XX AC AAU06175;

XX 24-OCT-2001 (first entry)

XX N. meningitidis EG329 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain EG329.

XX Key Location/Qualifiers

FT Region 1..50 /label= C1

FT /note= "Conserved region 1"

FT Region 51..108 /label= V1

FT /note= "Variable region 1"

FT Region 109..120 /label= C2

FT /note= "Conserved region 2"

FT Region 121..124 /label= V2

FT



Job time: 449 sec

```

XX N. meningitidis H41 Nhha deletion mutant.
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
XX Neisseria meningitidis strain H41.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT 1..51
FT Peptide /label= Signal_peptide
FT 52..513
FT Protein /label= Mature_Nhha_deletion_mutant
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
XX WO20015182-A1.
PN
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
PI
XX WPI: 2001-488774/53.
DR
DR N-PSDB; AAS091173.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 6; 9lpp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AA006182-AA006186) the modified mutant Nhha polypeptides are
CC characterised by deletions of non conserved amino acids particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain H41 surface
CC antigen Nhha deletion mutant.
XX
XX Sequence 513 AA;
SQ

Query Match 23.2%; Score 138; DB 22; Length 513;
Best Local Similarity 100.0%; Pred. No. 5,9e-127;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDNNVGDALNNVQLQNSGNLDSKAVAGSGKVISGNVSPSGKMDETVNINAGNNEIT 433
DB 293 YDNNVGDALNNVQLQNSGNLDSKAVAGSGKVISGNVSPSGKMDETVNINAGNNEIT 352
QY 434 RRGKNDITATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRITNVAPGVKE 493
DB 353 RRGKNDIATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRITNVAPGVKE 412
QY 494 GDVTNVQOLKGVAQNLLNN 511
DB 413 GDVTNVQOLKGVAQNLLNN 430

```

Search completed: September 5, 2002, 10:40:42



---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:36:54 ; Search time 25.54 Seconds  
(without alignments)  
568.082 Million cell updates/sec

Title: US-09-700-293-2

Perfect score: 594

Sequence: 1 MNKIYRIIWNALNAWAVS.....TASGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 2442594 residues

Word size : 20

Total number of hits satisfying chosen parameters: 39

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCrUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	100.0	594	4	US-09-377-155-9
2	594	100.0	594	4	US-09-669-974-9
3	161	27.1	591	4	US-09-377-155-11
4	161	27.1	591	4	US-09-377-155-21
5	161	27.1	591	4	US-09-669-974-11
6	161	27.1	591	4	US-09-669-974-21
7	161	27.1	592	4	US-09-377-155-2
8	161	27.1	592	4	US-09-669-974-2
9	138	23.2	589	4	US-09-377-155-19
10	138	23.2	589	4	US-09-669-974-19
11	138	23.2	592	4	US-09-377-155-17
12	138	23.2	592	4	US-09-669-974-17
13	138	23.2	598	4	US-09-377-155-5
14	138	23.2	598	4	US-09-377-155-13
15	138	23.2	598	4	US-09-669-974-5
16	138	23.2	598	4	US-09-669-974-13
17	94	15.8	599	4	US-09-377-155-15
18	94	15.8	599	4	US-09-669-974-15
19	93	15.7	594	4	US-09-377-155-7
20	93	15.7	594	4	US-09-669-974-7
21	23	3.9	658	1	US-08-409-995-5
22	23	3.9	658	3	US-08-685-467-5
23	23	3.9	658	4	US-08-913-942-5
24	23	3.9	1098	1	US-08-409-995-2
25	23	3.9	1098	3	US-08-685-467-2
26	23	3.9	1098	4	US-09-377-155-32
27	23	3.9	1098	4	US-08-913-942-2

28 23 3.9 1098 4 US-09-669-974-32 Sequence 32, Appl  
29 23 3.9 1098 4 US-09-268-347-44 Sequence 44, Appl  
30 22 3.7 1912 1 US-08-409-995-4 Sequence 4, Appl  
31 22 3.7 1912 3 US-08-685-467-4 Sequence 4, Appl  
32 22 3.7 2353 4 US-09-377-155-33 Sequence 33, Appl  
33 22 3.7 2353 4 US-08-913-942-4 Sequence 4, Appl  
34 22 3.7 2353 4 US-09-669-974-33 Sequence 33, Appl  
35 22 3.7 2354 4 US-09-268-347-47 Sequence 47, Appl  
36 22 3.7 2411 4 US-09-268-347-36 Sequence 36, Appl  
37 20 3.4 607 1 US-08-409-995-6 Sequence 6, Appl  
38 20 3.4 607 3 US-08-685-467-6 Sequence 6, Appl  
39 20 3.4 607 4 US-08-913-942-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match	100.0%	Score 594;	DB 4;	Length 594;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 594;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MNKYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE	60	
Db	1	MNKYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE	60	
Qy	61	PVQRTAVVLSFRSDKEGTEGTEVDSNMGVYFDKKGVLVTAGTITLKAGDNLKIKQNTNE	120	
Db	61	PVQRTAVVLSFRSDKEGTEGTEVDSNMGVYFDKKGVLVTAGTITLKAGDNLKIKQNTNE	120	
Qy	121	NTNASSFTYSLKCOLTDLTSVGTTEKLSFSANSKNVNIISDTKGLNPAKKAETNGDTTVH	180	
Db	121	NTNASSFTYSLKCOLTDLTSVGTTEKLSFSANSKNVNIISDTKGLNPAKKAETNGDTTVH	180	
Qy	181	LNGIGSTLDTLLNGATNTVNDVTDDEKKRAASVKDVLNAGWNIKVKPGCTASDNV	240	
Db	181	LNGIGSTLDTLLNGATNTVNDVTDDEKKRAASVKDVLNAGWNIKVKPGCTASDNV	240	
Qy	241	DFVRYDVEFLSADTKTTTVNVEKDKNGKRTVEVIGAKTSVKEKDKGLVFGDKGEND	300	
Db	241	DFVRYDVEFLSADTKTTTVNVEKDKNGKRTVEVIGAKTSVKEKDKGLVFGDKGEND	300	
Qy	301	SSTDKEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSGTNVTFASGKTGA	360	
Db	301	SSTDKEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSGTNVTFASGKTGA	360	
Qy	361	TVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKDE	420	
Db	361	TVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKDE	420	

```
QY 421 TVNINAGNIEITRNKKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480
DB 421 TVNINAGNIEITRNKKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480
QY 481 PVRITNVPAGVKEGDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQAYLPG 540
DB 481 PVRITNVPAGVKEGDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQAYLPG 540
QY 541 KSMMAIGGGTYRGEAGYAGIYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 KSMMAIGGGTYRGEAGYAGIYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 2
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 100.0%; Score 594; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNANVAVSELTRNHTKRASATVATVATLILFATVQASTDDDDLYLE 60
DB 1 MNKIYRIIWSALNANVAVSELTRNHTKRASATVATVATLILFATVQASTDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNMGVYFDKGVLTAGTITLKAGDNLKIKONTNE 120
DB 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNMGVYFDKGVLTAGTITLKAGDNLKIKONTNE 120
QY 121 NTNASSFTYSLKKDLTDLTSLVTEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGDTTVH 180
DB 121 NTNASSFTYSLKKDLTDLTSLVTEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGDTTVH 180
QY 181 LNGIGSTLTLTLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKPTTASDNV 240
DB 181 LNGIGSTLTLTLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKPTTASDNV 240
QY 241 DFVRTYDTEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDKGLVTGDKDGEND 300
DB 241 DFVRTYDTEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDKGLVTGDKDGEND 300
QY 301 SSTDKGELVTAKEVIDVANVAGWEMKTTTANGOTGOADKFEVTSCTNVTASGKGTGA 360
DB 301 SSTDKGELVTAKEVIDVANVAGWEMKTTTANGOTGOADKFEVTSCTNVTASGKGTGA 360
QY 361 TVSKDDOGNITVMYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKGKMD 420
DB 361 TVSKDDOGNITVMYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKGKMD 420
```

```
QY 421 TVNINAGNIEITRNKKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480
DB 421 TVNINAGNIEITRNKKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480
QY 481 PVRITNVPAGVKEGDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQAYLPG 540
DB 481 PVRITNVPAGVKEGDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQAYLPG 540
QY 541 KSMMAIGGGTYRGEAGYAGIYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 KSMMAIGGGTYRGEAGYAGIYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 3
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11

Query Match 27.1%; Score 161; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3,3e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDVANVAGWEMKTTTANGOTGOADKFEVTSCTNVTASGKGTATVSKD 365
DB 304 GEGLVTAKEVIDVANVAGWEMKTTTANGOTGOADKFEVTSCTNVTASGKGTATVSKD 363
QY 366 DQGNITVMYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKGKMDETVIN 425
DB 364 DQGNITVMYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKGKMDETVIN 423
QY 426 AGNIEITRNKKNIDIIATSMTPQFSSVSLGAGADAPTLSDV 466
DB 424 AGNIEITRNKKNIDIIATSMTPQFSSVSLGAGADAPTLSDV 464

RESULT 4
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
```

RESULT 6  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

	Query Match	27.1%	Score 161;	DB 4;	Length 592;
	Best Local Similarity	100.0%;	Pred. No.	3.3e-144;	
	Matches 161; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	306	GEGLVTAKEIVDAVNKAGWRMTTANGQTGQAOKFETVTSGTNVFASRGKTATVSKD	365		
Db	305	GEGLVTAKEIVDAVNKAGWRMTTANGQTGQAOKFETVTSGTNVFASRGKTATVSKD	364		
Ov	366	DGGNTVMYDVNVGDALNNVLONLNGWNLDLSKAVAGSSGKVVISGNVPSPKCKMDSETVIN	425		

```

; ORGANISM: Neisseria meningitidis
US-09-377-155-19

Query Match      23.2%  Score 138;  DB 4;  Length 589;
Best Local Similarity 100.0%;  Pred. No. 2e-122;
Matches 138;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 374 YDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIET 433
      |||
DB 369 YDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIET 428
      |||
QY 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRITNVAPGVKE 493
      |||
DB 429 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRITNVAPGVKE 488
      |||
QY 494 GDVTNVAQLKGVAQNLLN 511
      |||
DB 489 GDVTNVAQLKGVAQNLLN 506
      |||

RESULT 10
US-09-669-974-19
; Sequence 19, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match      27.1%  Score 161;  DB 4;  Length 592;
Best Local Similarity 100.0%;  Pred. No. 3.3e-144;
Matches 161;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 306 GEGLYTAKEVIDAVNKGWRMTTITANGQTQADKFTVTSNGTNVTFASGKGTATVSKD 365
      |||
DB 305 GEGLYTAKEVIDAVNKGWRMTTITANGQTQADKFTVTSNGTNVTFASGKGTATVSKD 364
      |||
QY 366 DQGNITVYDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNI 425
      |||
DB 365 DQGNITVYDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNI 424
      |||
QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
      |||
DB 425 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 465
      |||

RESULT 9
US-09-377-155-19
; Sequence 19, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
```

```

; ORGANISM: Neisseria meningitidis
US-09-377-155-19

Query Match      23.2%  Score 138;  DB 4;  Length 589;
Best Local Similarity 100.0%;  Pred. No. 2e-122;
Matches 138;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 374 YDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIET 433
      |||
DB 369 YDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIET 428
      |||
QY 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRITNVAPGVKE 493
      |||
DB 429 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRITNVAPGVKE 488
      |||
QY 494 GDVTNVAQLKGVAQNLLN 511
      |||
DB 489 GDVTNVAQLKGVAQNLLN 506
      |||

RESULT 11
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
```

Query Match	23.2%	Score 138;	DB 4;	Length 592;
Best Local Similarity	100.0%;	Pred. No. 2e-122;		
Matches 138;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	374	YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVTSGNVSPSKGKMDETVTNINAGNNIET	433	
Db	372	YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVTSGNVSPSKGKMDETVTNINAGNNIET	431	
Qy	434	RNGKNIDIATSWTQPFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRTNVPAGVKE	493	
Db	432	RNGKNIDIATSWTQPFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRTNVPAGVKE	491	

```

RESULT 14
US-09-377-155-13
> Sequence 13, Application US/09377155
> Patent NO. 6197312
> GENERAL INFORMATION:
> APPLICANT: PEAK, Ian Richard Anselm
> APPLICANT: JENNINGS, Michael Paul
> APPLICANT: MOXON, E. Richard
> TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
> FILE REFERENCE: 065064/0128
> CURRENT APPLICATION NUMBER: US/09/377,155
> CURRENT FILING DATE: 1999-08-19
> PRIOR APPLICATION NUMBER: PCT/AU98/01031
> PRIOR FILING DATE: 1998-12-14
> PRIOR APPLICATION NUMBER: GB 9726398.2
> PRIOR FILING DATE: 1997-12-12
> NUMBER OF SEQ ID NOS: 33
> SOFTWARE: PatentIn ver. 2.0
> SEQ ID NO 13
> LENGTH: 598
> TYPE: PRT
> ORGANISM: Neisseria meningitidis
US-09-377-155-13

```

Query Match 23.2%; Score 138; DB 4; Length 598;

Best Local Similarity	100.0%;	Pred. No. 2e-122;	
Matches 138;	Conservative	0;	Mismatches 0;
			Indels 0;
			Gaps 0;

Qy	374	YDYNVGDALNVNQQLONGSNWLDKSAKVAGSSKVKVTSIGNVSPSKGKMDETVTNINAGNNITET	433
Db	378	YDYNVGDALNVNQQLONGSNWLDKSAKVAGSSKVKVTSIGNVSPSKGKMDETVTNINAGNNITET	437
Qy	434	RNGKNIDIATSMTPQFSSVSLGAGADAPPTLSVDDEGALNMGSKDKANKPVRITTNVAPGVKE	493
Db	438	RNGKNIDIATSMTPQFSSVSLGAGADAPPTLSVDDEGALNMGSKDKANKPVRITTNVAPGVKE	497
Qy	494	GDTVNTVAOLKGVAQNLLN	511
Db	498	GDTVNTVAOLKGVAQNLLN	515

```

RESULT 15
US-09-669-974-5
  ? Sequence 5, Application US/09669974
  ? Patent No. 633173
  ? GENERAL INFORMATION:
  ?
  ? APPLICANT: JENKINS, Ian Richard Anselm
  ? APPLICANT: PEARNS, Michael Paul
  ? APPLICANT: MOXON, E. Richard
  ? TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
  ? FILE REFERENCE: 065064/01128
  ? CURRENT APPLICATION NUMBER: US/09/669,974
  ? CURRENT FILING DATE: 2000-09-26
  ? PRIOR APPLICATION NUMBER: US 09/377,155
  ? PRIOR FILING DATE: 1998-08-19
  ? PRIOR APPLICATION NUMBER: PCT/AY98/01031
  ? PRIOR FILING DATE: 1998-12-14
  ? PRIOR APPLICATION NUMBER: GB 9726398.2
  ? PRIOR FILING DATE: 1997-12-12
  ? NUMBER OF SEQ ID NOS: 33
  ? SOFTWARE: PatentIn Ver. 2.0
  ? SEQ ID NO 5
  ? LENGTH: 598
  ? TYPE: PRT
  ? ORGANISM: Neisseria meningitidis
US-09-669-974-5

```

Query Match 23.2%; Score 138; DB 4; Length 598;  
Best Local Similarity 100.0%; Pred. No. 2e-122;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Search completed: September 5, 2002, 10:41:15  
Job time: 261 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:38:14 ; Search time 33.9 Seconds  
(without alignments)  
1683.689 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNALNAWVAYS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	27.1	591	2 G81133	adhesin NMB0992 [i
2	127	21.4	592	2 A81888	probable surface f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TET>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAFA1395.1; PID:g722623  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 8.7e-156;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSCTNVTFFASGKGTATVSKD 365  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSCTNVTFFASGKGTATVSKD 363  
Qy 366 DOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNTIN 425  
Db 364 DOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNTIN 423  
Qy 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTILSVD 466  
Db 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTILSVD 464

RESULT 2

A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match 21.4%; Score 127; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 5e-121;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSCTNVTFFASGKGTATVSKD 365  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSCTNVTFFASGKGTATVSKD 363  
Qy 366 DOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNTIN 425  
Db 364 DOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNTIN 423  
Qy 426 AGNNIEI 432  
Db 424 AGNNIEI 430

Search completed: September 5, 2002, 10:41:54  
Job time: 220 sec

Thu Sep 5 14:35:54 2002

us-09-700-293-2.oligo20.rpr

Page 2

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:41:19 ; Search time 19.15 Seconds  
(without alignments)  
1201.014 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNALNAWVYS.....TASGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
---------------	-------	----------------	--------	-------	-------------

No matches found

Search completed: September 5, 2002, 10:48:19  
Job time: 420 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:40:49 ; Search time 55.95 Seconds  
(without alignments)  
1836.622 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNALNAWVVS.....TASGNSRGHFGASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 20

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	594	100.0	594	2 Q93QY4	Q93qy4 neisseria m
2	221	37.2	594	2 Q9JP13	Q9jpi3 neisseria m
3	221	37.2	594	2 Q9JPS2	Q9jps2 neisseria m
4	221	37.2	594	2 Q9JPH0	Q9jph0 neisseria m
5	162	27.3	592	2 Q9JPS9	Q9jps9 neisseria m
6	162	27.3	598	2 Q9JPR7	Q9jpr7 neisseria m
7	162	27.3	599	2 Q9JPS8	Q9jps8 neisseria m
8	161	27.1	591	2 Q9JPS7	Q9jps7 neisseria m
9	161	27.1	591	2 Q93QX3	Q93qy3 neisseria m
10	161	27.1	591	16 Q9JRI8	Q9jri8 neisseria m
11	161	27.1	592	2 Q9AQF0	Q9aqf0 neisseria m
12	138	23.2	589	2 Q9JPI0	Q9jpi0 neisseria m
13	138	23.2	589	2 Q93QY1	Q93qy1 neisseria m
14	138	23.2	590	2 Q9JPS3	Q9jps3 neisseria m
15	138	23.2	592	2 Q93QX2	Q93qy2 neisseria m
16	138	23.2	598	2 Q9JPT0	Q9jpt0 neisseria m

17 138 23.2 598 2 Q9JPS0 Q9jps0 neisseria m  
18 138 23.2 598 2 Q93QY5 Q93qy5 neisseria m  
19 138 23.2 600 2 Q9JPS5 Q9jps5 neisseria m  
20 127 21.4 592 16 Q9JQW4 Q9jqw4 neisseria m  
21 94 15.8 599 2 Q9JPR8 Q9jpr8 neisseria m  
22 93 15.7 526 2 Q9JPS4 Q9jps4 neisseria m  
23 93 15.7 530 2 Q9JPS1 Q9jps1 neisseria m  
24 93 15.7 594 2 Q9JPH7 Q9jph7 neisseria m  
25 93 15.7 598 2 Q9JPR9 Q9jpr9 neisseria m  
26 93 15.7 600 2 Q9JPS6 Q9jps6 neisseria m  
27 23 3.9 1098 2 Q48152 Q48152 haemophilus  
28 22 3.7 2353 2 P71401 P71401 haemophilus

ALIGNMENTS

RESULT 1  
Q93QY4  
ID Q93QY4 PRELIMINARY; PRT; 594 AA.  
AC Q93QY4;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG327;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157605; AAK68866.1; -  
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 100.0%; Score 594; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATAVLATLLEFATVQASTTDDDDLYLE 60  
|||||  
Db 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATAVLATLLEFATVQASTTDDDDLYLE 60  
Qy 61 PVQRTAVVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
|||||  
Db 61 PVQRTAVVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Qy 121 NTNASSFTYSLKKDLTDLTSVGTETKLSFSANSKNKNVITSDTKGLNFAKTAETNGDTTVH 180  
|||||  
Db 121 NTNASSFTYSLKKDLTDLTSVGTETKLSFSANSKNKNVITSDTKGLNFAKTAETNGDTTVH 180  
Qy 181 LINGIGSTLDTLLNGATTNTNDVNTDDEKKRAASVKDVLNAGNKGKPGTTASDNV 240  
|||||  
Db 181 LINGIGSTLDTLLNGATTNTNDVNTDDEKKRAASVKDVLNAGNKGKPGTTASDNV 240  
Qy 241 DVRTYDTVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIKEKDKGLVTGDKGEND 300  
Db 241 DVRTYDTVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIKEKDKGLVTGDKGEND 300  
Qy 301 SSTDKGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTASGKGTTA 360  
|||||  
Db 301 SSTDKGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTASGKGTTA 360  
Qy 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420  
Db 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420  
Qy 421 TVNINAGNIEITRNGKNIDIATSMTPQPSVSLGAGADAPTLSDVDEGALNVGSKDANK 480

```
Db 421 TVNINAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480
QY 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPG 540
Db 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPG 540
QY 541 KSMAIGGGTYRGEAGYATGYSSISDGGNWIITKGTASGNSRHFSGASASVGVQW 594
Db 541 KSMAIGGGTYRGEAGYATGYSSISDGGNWIITKGTASGNSRHFSGASASVGVQW 594

RESULT 2
Q9JPI3 ID Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3
DT 01-OCT-2000 (TremBLrel. 15, Created)
DR 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RC STRAIN=NG3/88, AND BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226369; AAF42518.1; -.
DR EMBL: AF226369; AAF42518.1; -.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 37.2%; Score 221; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 4e-204;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDENVGDLNVQLNSGNWLDKSAVAGSSGKVISGNVSPSKGMDVTNINAGNNIET 433
Db 374 YDENVGDLNVQLNSGNWLDKSAVAGSSGKVISGNVSPSKGMDVTNINAGNNIET 433
QY 434 RKGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
Db 434 RKGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
QY 494 GDVTNVQALKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPGSKSMAIGGGTYRG 553
Db 494 GDVTNVQALKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPGSKSMAIGGGTYRG 553
QY 554 EAGYATGYSSISDGGNWIITKGTASGNSRHFSGASASVGVQW 594
Db 554 EAGYATGYSSISDGGNWIITKGTASGNSRHFSGASASVGVQW 594

RESULT 3
Q9JPS2 ID Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2
DT 01-OCT-2000 (TremBLrel. 15, Created)
DR 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
```

```
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR EMBL: AF226379; AAF42528.1; -.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F5D3D256 CRC64;

Query Match 37.2%; Score 221; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 4e-204;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDENVGDLNVQLNSGNWLDKSAVAGSSGKVISGNVSPSKGMDVTNINAGNNIET 433
Db 374 YDENVGDLNVQLNSGNWLDKSAVAGSSGKVISGNVSPSKGMDVTNINAGNNIET 433
QY 434 RKGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
Db 434 RKGKNIDATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
QY 494 GDVTNVQALKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPGSKSMAIGGGTYRG 553
Db 494 GDVTNVQALKGVAQNLNHNIDNVGNARAGIAQAIAATAGLVQAYLPGSKSMAIGGGTYRG 553
QY 554 EAGYATGYSSISDGGNWIITKGTASGNSRHFSGASASVGVQW 594
Db 554 EAGYATGYSSISDGGNWIITKGTASGNSRHFSGASASVGVQW 594

RESULT 4
Q9JPH0 ID Q9JPH0 PRELIMINARY; PRT; 595 AA.
AC Q9JPH0
DT 01-OCT-2000 (TremBLrel. 15, Created)
DR 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RC STRAIN=528, AND 1000;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226360; AAF42509.1; -.
DR EMBL: AF226360; AAF42509.1; -.
DR EMBL: AF226360; AAF42509.1; -.
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;
```

```
Query Match 37.2%; Score 221; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 4e-204;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 YDNNVGDALNNQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDVTNINAGNNIEIT 433
Dy 375 YDNNVGDALNNQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDVTNINAGNNIEIT 434
Qy 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRTTNNVAPGVKE 493
Dy 435 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRTTNNVAPGVKE 494
Qy 494 GDVTNVAOLKGAQNLNHNDVGNARAGIAQAIAATAGLVAOYLPGKSMMAIGGTYRG 553
Dy 495 GDVTNVAOLKGAQNLNHNDVGNARAGIAQAIAATAGLVAOYLPGKSMMAIGGTYRG 554
Qy 554 EAGVAIGYSSISDGNWIIKGTASGNSRGHGASASVGYQW 594
Dy 555 EAGVAIGYSSISDGNWIIKGTASGNSRGHGASASVGYQW 595

RESULT 5
Q9JPS9 PRELIMINARY; PRT; 592 AA.
AC Q9JPS9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=860809;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 27.3%; Score 162; DB 2; Length 592;
Best Local Similarity 100.0%; Pred. No. 3e-147;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKTTATVSKD 365
Dy 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKTTATVSKD 363
Qy 366 DOGNITVMYDNNVGDALNNQNSGNLDSKAVAGSSGKVISGNVSPSKGMDVTNIN 425
Dy 364 DOGNITVMYDNNVGDALNNQNSGNLDSKAVAGSSGKVISGNVSPSKGMDVTNIN 423
Qy 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDD 467
Dy 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDD 465

RESULT 6
Q9JPR7 PRELIMINARY; PRT; 598 AA.
AC Q9JPR7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
```

```
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SWZ107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226385; AAF42534.1; -.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 27.3%; Score 162; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 3e-147;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKTTATVSKD 365
Dy 310 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKTTATVSKD 369
Qy 366 DOGNITVMYDNNVGDALNNQNSGNLDSKAVAGSSGKVISGNVSPSKGMDVTNIN 425
Dy 370 DOGNITVMYDNNVGDALNNQNSGNLDSKAVAGSSGKVISGNVSPSKGMDVTNIN 429
Qy 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDD 467
Dy 430 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDD 471

RESULT 7
Q9JPS8 PRELIMINARY; PRT; 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42513.1; -.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 27.3%; Score 162; DB 2; Length 599;
```

Best Local Similarity 100.0%; Pred. No. 3e-147;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSVSGTNTVFASGKGTATVSKD 365  
|||||  
Db 311 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSVSGTNTVFASGKGTATVSKD 370  
|||||  
QY 366 DQGNITVMDVNYGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDVTNIN 425  
|||||  
Db 371 DQGNITVMDVNYGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDVTNIN 430  
|||||  
QY 426 AGNNIEITRNKKNIDATSMTPQFSSVSLGAGADAPTLSD 467  
|||||  
Db 431 AGNNIEITRNKKNIDATSMTPQFSSVSLGAGADAPTLSD 472  
|||||

RESULT 8  
Q9JPS7 PRELIMINARY; PRT; 591 AA.  
ID Q9JPS7  
AC 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN Neisseria meningitidis.  
OS Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OC NCBI\_TaxID=487;  
OX [1]  
RN  
RP  
RC  
RX STRAIN=B2147;  
MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of vaccine candidates against serogroup B  
Meningococcus by whole-genome sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1; --  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.7e-146;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSVSGTNTVFASGKGTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSVSGTNTVFASGKGTATVSKD 363  
|||||  
QY 366 DQGNITVMDVNYGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDVTNIN 425  
|||||  
Db 364 DQGNITVMDVNYGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDVTNIN 423  
|||||  
QY 426 AGNNIEITRNKKNIDATSMTPQFSSVSLGAGADAPTLSD 466  
|||||  
Db 424 AGNNIEITRNKKNIDATSMTPQFSSVSLGAGADAPTLSD 464  
|||||

RESULT 9  
Q93QY3 PRELIMINARY; PRT; 591 AA.  
ID Q93QY3  
AC 093QY3  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.

Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OC NCBI\_TaxID=487;  
OX [1]  
RN  
RP  
RC  
RX STRAIN=EG329;  
MEDLINE=20175756; PubMed=10710308;  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of vaccine candidates against serogroup B  
Meningococcus by whole-genome sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF157606; AAK68867.1; --  
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.7e-146;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSVSGTNTVFASGKGTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTSVSGTNTVFASGKGTATVSKD 363  
|||||  
QY 366 DQGNITVMDVNYGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDVTNIN 425  
|||||  
Db 364 DQGNITVMDVNYGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDVTNIN 423  
|||||  
QY 426 AGNNIEITRNKKNIDATSMTPQFSSVSLGAGADAPTLSD 466  
|||||  
Db 424 AGNNIEITRNKKNIDATSMTPQFSSVSLGAGADAPTLSD 464  
|||||

RESULT 10  
Q9JR18 PRELIMINARY; PRT; 591 AA.  
ID Q9JR18  
AC 09JR18  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE  
PROTEIN).  
GN GNA992 OR NMB0992 OR NHHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
RP  
RC  
RX STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;  
MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of vaccine candidates against serogroup B  
Meningococcus by whole-genome sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1; --  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;



```

[3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -
DR EMBL; AE002450; AAF41395.1; -
DR EMBL; AF226367; AAF42516.1; -
DR EMBL; AF226370; AAF42519.1; -
DR EMBL; AF226374; AAF42523.1; -
DR EMBL; AF157611; AAK68872.1; -
DR TIGR; NMB0992; -
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAEF7F73EC6 CRC64;

Query Match 27.1%; Score 161; DB 16; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEETVTSGTNVTASGKGTATVSKD 365
Db 304 GEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEETVTSGTNVTASGKGTATVSKD 363

QY 366 DQGNITVMYDVNGDALNVNQLNSGWNLDKAVAGSGKVIISGNVSPSKGMDETVNN 425
Db 364 DQGNITVMYDVNGDALNVNQLNSGWNLDKAVAGSGKVIISGNVSPSKGMDETVNN 423

QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
Db 424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464

RESULT 11
Q9AQF0 PRELIMINARY; PRT; 592 AA.
ID Q9AQF0
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 27.1%; Score 161; DB 2; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEETVTSGTNVTASGKGTATVSKD 365
Db 305 GEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEETVTSGTNVTASGKGTATVSKD 364

QY 366 DQGNITVMYDVNGDALNVNQLNSGWNLDKAVAGSGKVIISGNVSPSKGMDETVNN 425
Db 365 DQGNITVMYDVNGDALNVNQLNSGWNLDKAVAGSGKVIISGNVSPSKGMDETVNN 424

QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
Db 425 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 465
```

```

RESULT 12
Q9JPI0 PRELIMINARY; PRT; 589 AA.
ID Q9JPI0
AC Q9JPI0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGP155, 90/18311, AND 93/4286;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
  Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226384; AAF42533.1; -
DR EMBL; AF226362; AAF42511.1; -
DR EMBL; AF226363; AAF42512.1; -
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95D4868566A6 CRC64;

Query Match 23.2%; Score 138; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDKAVAGSGKVIISGNVSPSKGMDETVNNAGNIEIT 433
Db 369 YDVNVGDALNVNQLNSGWNLDKAVAGSGKVIISGNVSPSKGMDETVNNAGNIEIT 428

QY 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGYKE 493
Db 429 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGYKE 488

QY 494 GDVTNVAQLKGVQNLNN 511
Db 489 GDVTNVAQLKGVQNLNN 506

RESULT 13
Q93QY1 PRELIMINARY; PRT; 589 AA.
ID Q93QY1
AC Q93QY1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P20;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157610; AAK68871.1; -
SQ SEQUENCE 589 AA; 61448 MW; 1F1A80CD610CB230 CRC64;
```

Query Match 23.2%; Score 138; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 4e-124;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDKMTVNVNAGNNIEIT 433  
|||||  
Db 369 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDKMTVNVNAGNNIEIT 428  
QY 434 RKGKNIIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
|||||  
Db 429 RKGKNIIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 488  
QY 494 GDVTNVAQLKGVAQNINN 511  
|||||  
Db 489 GDVTNVAQLKGVAQNINN 506  
|||||

RESULT 14

ID Q9JPS3 PRELIMINARY; PRT; 590 AA.  
AC Q9JPS3;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storti E., Zuppi,  
RA Broeker M., Hundt E., Knapp B., Blait E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole Genome Sequencing.";  
RL Science 297:1816-1820(2000).  
DR EMBL; AF226378; AAF42527.1; -.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 23.2%; Score 138; DB 2; Length 590;  
Best Local Similarity 100.0%; Pred. No. 4e-124;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDKMTVNVNAGNNIEIT 433  
|||||  
Db 370 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDKMTVNVNAGNNIEIT 429  
QY 434 RKGKNIIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
|||||  
Db 430 RKGKNIIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 489  
QY 494 GDVTNVAQLKGVAQNINN 511  
|||||  
Db 490 GDVTNVAQLKGVAQNINN 507  
|||||

RESULT 15

ID Q93QY2 PRELIMINARY; PRT; 592 AA.  
AC Q93QY2;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.

GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4;  
RX Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DDJB databases.  
DR EMBL; AF157609; AAK68870.1; -. F9403A0B4A18EEA7 CRC64;  
SQ SEQUENCE 592 AA; 61869 MW; 61869 MW; F9403A0B4A18EEA7 CRC64;

Query Match 23.2%; Score 138; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 4e-124;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDKMTVNVNAGNNIEIT 433  
|||||  
Db 372 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDKMTVNVNAGNNIEIT 431  
QY 434 RKGKNIIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
|||||  
Db 432 RKGKNIIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 491  
QY 494 GDVTNVAQLKGVAQNINN 511  
|||||  
Db 492 GDVTNVAQLKGVAQNINN 509  
|||||

Search completed: September 5, 2002, 10:47:55  
Job time: 426 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:14 ; Search time 58.56 Seconds  
(without alignments)  
1120.980 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MKKIYRIIWNLSALNAWVAYS.....TASGNSRGHFGASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2999	99.9	591	AAV27202	Amino acid sequenc
2	2999	99.9	591	AAV23746	A surface protein
3	2999	99.9	591	AAU06171	N. meningitidis PM
4	2981	99.3	591	AAV57045	BAS029 amino acid
5	2980	99.2	591	AAU23741	A surface protein
6	2980	99.2	591	AAU06175	N. meningitidis EG
7	2967.5	98.8	592	AAV23737	A surface protein
8	2762.5	92.0	594	AAV23740	A surface protein
9	2762.5	92.0	594	AAV57044	BAS029 amino acid
10	2762.5	92.0	594	AAU06174	N. meningitidis EG
11	2736.5	91.1	594	AAV23739	A surface protein

12	2736.5	91.1	594	22	AAU06179	N. meningitidis B2
13	2721.5	90.6	598	20	AAV23742	A surface protein
14	2721.5	90.6	598	22	AAU06177	N. meningitidis H1
15	2712.5	90.3	598	20	AAV23738	A surface protein
16	2712.5	90.3	598	22	AAU06178	N. meningitidis B2
17	2689	89.5	599	20	AAV23743	A surface protein
18	2689	89.5	599	22	AAU06176	N. meningitidis H3
19	2577.5	85.8	592	20	AAV23744	A surface protein
20	2577.5	85.8	592	22	AAU06172	N. meningitidis H4
21	2546.5	84.8	512	22	AAU06182	N. meningitidis PM
22	2475	82.4	589	20	AAV23745	A surface protein
23	2475	82.4	589	22	AAU06173	N. meningitidis P2
24	2468.5	82.2	592	22	AAU06180	N. meningitidis Z2
25	2455.5	81.8	502	22	AAU06186	N. meningitidis PM
26	2439.5	81.2	592	20	AAV27203	Amino acid sequenc
27	2411	80.3	513	22	AAU06183	N. meningitidis H4
28	2231.5	74.3	604	22	AAU06181	N. meningitidis su
29	2104	70.1	433	22	AAU06185	N. meningitidis PM
30	1957	65.2	407	22	AAU06184	N. meningitidis PM
31	1245	41.5	2411	21	AAU23860	Haemophilus influe
32	1243	41.4	2353	17	AAV93933	Haemophilus adhesi
33	1228	40.9	245	20	AAV27201	Amino acid sequenc
34	1070.5	35.6	1094	21	AAU23858	Haemophilus influe
35	1057.5	35.2	1098	17	AAV93932	Haemophilus adhesi
36	995	33.1	679	17	AAV93934	Haemophilus adhesi
37	995	33.1	679	21	AAU23855	Haemophilus influe
38	752.5	25.1	1004	21	AAU23857	Haemophilus influe
39	741.5	24.7	1002	21	AAU23854	Haemophilus influe
40	696.5	23.2	1104	21	AAU23856	Haemophilus influe
41	696.5	23.2	1104	21	AAU23859	Haemophilus influe
42	600	20.0	116	21	AAU37832	Neisserial conserv
43	388	12.9	2314	22	AAU69136	M. catarrhalis les
44	386.5	12.9	1778	22	AAU52677	Escherichia coli p
45	382	12.7	2123	22	AAU00701	Moraxella catarrha

ALIGNMENTS

RESULT 1  
AAV27202  
ID AAV27202 standard; Protein; 591 AA.  
AC AAV27202;  
DT 24-SEP-1999 (first entry)  
XX  
XX  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX  
XX  
OS Neisseria meningitidis.  
XX  
XX  
PN WO9936544-A2.  
XX  
XX  
PD 22-JUL-1999.  
XX  
XX  
PF 14-JAN-1999; 99WO-IB00103.  
XX  
XX  
PR 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX (CHIR-) CHIRON SPA.  
PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
XX WPI: 1999-444400/37.  
DR N-PSDB; AAU99124.  
XX  
XX  
PT New protein and its nucleotide sequence, useful in vaccines or  
diagnostic compositions for treating and/or preventing Neisseria

PT meningitidis infections  
XX Claim 1; Page 62; 123pp; English.  
XX The invention provides proteins (AA27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AA29123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
XX Sequence 591 AA;  
SQ  
  
Query Match 99.9%; Score 2999; DB 20; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.9e-171;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60  
DB 1 mnkiyriiwsalnawvvvseltrnhtkrasatvktavlatllifatvqasannee 60  
  
QY 61 YLDPVQRTAVLIVNSDKGTEGKEKVEKVEKVEKVEKVEKVEKVEKVEKVEKVEK 120  
DB 61 yldpqrtvavllivnsdkgtegekveekveekveekveekveekveekveek 120  
  
QY 121 NGTFYSLAKDLTDLTSVGTSEKLSFSAANGKVNITSDTKLNFPAKETAGTGTTHLN 180  
DB 121 ngtnftyslkkdltdltsvgtseklslfsangknvntsdtklnfaketa 180  
  
QY 181 GIGSTLDTLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIGVKPGTASNDVDF 240  
DB 181 gisgltldtllntgattntndvtddekkraasvkdvlmagwnigvpgt 240  
  
QY 241 VRTYDTVEFLSADTKTTTVNVEKDKGKTEVIGAKTSVKEKDKGLVTKGDKGENSS 300  
DB 241 vrttydtveflsadtktttvnveskdkgkteviga ktsvkekdglv 300  
  
QY 301 TDEGEGLVTAKEVIDAVNKGWRMKTITTTANGQTQADKFETVTSNVTFSAGKGTATV 360  
DB 301 tdegeglvtakevidavnkgwrmttttangqtqadkfetvtsnvtf 360  
  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSGKVGISGNVSPSKGMD 420  
DB 361 skddqgnitvmydvnvgdalnv nqlqnsqwnldskavagsgkv 420  
  
QY 421 NINAGNIEITRNGKNIDTATSMTPQFSVSLGAGADAPTLSDGDALNVGSKDKNKPVR 480  
DB 421 ninagnieitrngknidiat smtpqfssvslgagadap 480  
  
QY 481 ITNVAPGVKGGDVTVNAQLKGYAQLNLRIDNVGNARAGIAQAIATAGLVQAYLP 540  
DB 481 itnvapgvkggdvtvnaqlkgyaqlnlridnvgnarag 540  
  
QY 541 MAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 591  
DB 541 maigggtyrgeagayagysis dgggniikgtasgnsrghfg 591  
  
RESULT 2  
AA23746  
ID AA23746 standard; Protein; 591 AA.  
XX  
AC AA23746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of *Neisseria meningitidis*.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX

OS *Neisseria meningitidis*.  
XX WO9931132-A1.  
XX PD 24-JUN-1999.  
XX PF 14-DEC-1998; 98WO-AU01031.  
XX PR 12-DEC-1997; 97GB-0026398.  
XX (ISIS-) ISIS INNOVATION LTD.  
XX (UYQU) UNIV QUEENSLAND.  
XX Jennings MP, Moxon ER, Peak IRA;  
XX WPI; 1999-418754/35.  
XX N-PSDB; AAX85798.  
XX *Neisseria meningitidis* surface proteins useful for treating *N.*  
XX meningitidis infections  
XX Claim 1; Page 127-128; 132pp; English.  
XX The present sequence represents a surface protein of *Neisseria*  
XX meningitidis which is approximately 62 kDa. The *N. meningitidis*  
XX surface glycoproteins, nucleic acids, the primers and optionally  
XX a thermostable polymerase, or antibodies are useful in a kit for  
XX the detection or diagnosis of *N. meningitidis* infection in humans.  
XX The *N. meningitidis* surface glycoproteins can also be used to  
XX prevent or treat *N. meningitidis* infection in humans, especially  
XX in the form of vaccines. The proteins and antibodies can also  
XX be used to identify immunoreactive peptides.  
XX Sequence 591 AA;  
SQ  
  
Query Match 99.9%; Score 2999; DB 20; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.9e-171;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60  
DB 1 mnkiyriiwsalnawvvvseltrnhtkrasatvktavlatllifatvqasannee 60  
  
QY 61 YLDPVQRTAVLIVNSDKGTEGKEKVEKVEKVEKVEKVEKVEKVEKVEKVEKVEK 120  
DB 61 yldpqrtvavllivnsdkgtegekveekveekveekveekveekveekveek 120  
  
QY 121 NGTFYSLAKDLTDLTSVGTSEKLSFSAANGKVNITSDTKLNFPAKETAGTGTTHLN 180  
DB 121 ngtnftyslkkdltdltsvgtseklslfsangknvntsdtklnfaketa 180  
  
QY 181 GIGSTLDTLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIGVKPGTASNDVDF 240  
DB 181 gisgltldtllntgattntndvtddekkraasvkdvlmagwnigvpgt 240  
  
QY 241 VRTYDTVEFLSADTKTTTVNVEKDKGKTEVIGAKTSVKEKDKGLVTKGDKGENSS 300  
DB 241 vrttydtveflsadtktttvnveskdkgkteviga ktsvkekdglv 300  
  
QY 301 TDEGEGLVTAKEVIDAVNKGWRMKTITTTANGQTQADKFETVTSNVTFSAGKGTATV 360  
DB 301 tdegeglvtakevidavnkgwrmttttangqtqadkfetvtsnvtf 360  
  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSGKVGISGNVSPSKGMD 420  
DB 361 skddqgnitvmydvnvgdalnv nqlqnsqwnldskavagsgkv 420  
  
QY 421 NINAGNIEITRNGKNIDTATSMTPQFSVSLGAGADAPTLSDGDALNVGSKDKNKPVR 480  
DB 421 ninagnieitrngknidiat smtpqfssvslgagadap 480  
  
QY 481 ITNVAPGVKGGDVTVNAQLKGYAQLNLRIDNVGNARAGIAQAIATAGLVQAYLP 540  
DB 481 itnvapgvkggdvtvnaqlkgyaqlnlridnvgnarag 540  
  
QY 541 MAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 591  
DB 541 maigggtyrgeagayagysis dgggniikgtasgnsrghfg 591

Db 481 itnvapgvkegvdtnvaqlkgvaqlnnrldnvdgnaragiagataglvqaylpgksm 540  
 QY 541 MAIGGTYRGEAGYAGYSSISDGNWIKGTASGNSRCHFGASASVGYQW 591  
 Db 541 maigggtyrgeagyaigyssisdggnwllkgtasgnsrghfgasasvgyqw 591

## RESULT 3

AAU06171  
 ID AAU06171 standard; Protein; 591 AA.  
 AC AAU06171;  
 XX  
 XX 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.  
 XX  
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain PMC21.  
 XX

Key	Location/Qualifiers
Peptide	1..51
Region	/label= Signal_peptide 1..50
Region	/label= C1 /note= "Conserved region 1"
Region	51..108 /label= V1 /note= "Variable region 1"
Protein	52..591 /label= Mature_Nhha /note= "Predicted mature protein, specifically claimed in claim 12"
Region	109..120 /label= C2 /note= "Conserved region 2"
Region	121..124 /label= V2 /note= "Variable region 2"
Region	125..188 /label= C3 /note= "Conserved region 3"
Region	189..210 /label= V3 /note= "Variable region 3"
Region	211..229 /label= C4 /note= "Conserved region 4"
Region	230..236 /label= V4 /note= "Variable region 4"
Region	237..591 /label= C5 /note= "Conserved region 5"

WO200155182-A1.

02-AUG-2001.

25-JAN-2001; 2001WO-AU00069.

25-JAN-2000; 2000US-0177917.

(UYOU ) UNIV QUEENSLAND.

Peak IRA, Jennings MP;

WPI: 2001-488774/53.

N-PSDB; AAS09161.

PT New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 9; Fig 1; 9lpp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 XX the present invention.  
 SQ Sequence 591 AA;

Query Match 99.9%; Score 2999; DB 22; Length 591;

Best Local Similarity 99.8%; Pred. No. 1.9e-171;

Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLILFATVQASANNEEEDL 60

Db 1 mnkiyriwnsalnawvsvseltrnhtkrasatvktavlatlilfatvqasanneeedl 60

QY 61 YLDPVORTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120

Db 61 yldpvortvavlivnsdkegtgekekeveensdwavfnekgvltareitlkagdnlikq 120

QY 121 NCTNFTYSLKDLTLTSVGTSEKLSFANGKNVNIITSDTKGLNFAKETAGTNGDTTTHLN 180

Db 121 ngtnftyslkdltdltsvgteklfsangknvniitstdtkglnfaketagngdtthln 180

QY 181 GIGSTLTDLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNKGVKPGTTASNDVF 240

Db 181 gigstltdllntgattntvndvdekkraasvkdvlmagwnlkgvpgttasndvf 240

QY 241 VRTYDTVEFLSADTKTTTVNESKDKGKTEVKIGAKTSVIREKDKLVTGDKKGNGSS 300

Db 241 vrtvdtveflsadtktttvnveskdngkktevkigaktsvirekdklvtgdkkgngss 300

QY 301 TDEGEGLVTAKEVIDAVNKAGWRMKTTHANGQTQADKFETVTSGTNTVTFASGKGTATV 360

Db 301 tdegeglvtakevidavnkagwrmkthtngqgqadkfetvtsgntvtfasgkgtatv 360

QY 361 SKDDQGNITVMYDNNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSGKMDIV 420

Db 361 skddqgnitvmymydvngdnlvnglqnsqwnldskavagssgkvisgnvpsgkmdetv 420

QY 421 NINAGNIEITRNGKNIDIATSMTPQFSSVSLCAGADAPTSLVDGALNVGSKDKNKPVR 480

Db 421 ninagnieitrngknidiatsmtpfssvslcagadaptslvdgalnvsgkdknkpvr 480

QY 481 ITNAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGNARAGIAQAATAGLVQAYLPKSM 540

Db 481 itnappgvkegdvtnvaqlkgvaqlnnrldnvdgnaragiagataglvqaylpgksm 540

QY 541 MAIGGTYRGEAGYAGYSSISDGNWIKGTASGNSRCHFGASASVGYQW 591

Db 541 maigggtyrgeagyaigyssisdggnwllkgtasgnsrghfgasasvgyqw 591

## RESULT 4

AAU57045

ID AAU57045 standard; Protein; 591 AA.

XX

AC AAU57045;

XX 21-FEB-2000 (first entry)  
 XX BASB029 amino acid sequence from N. meningitidis strain H44/76.  
 XX BASB029: *Neisseria meningitidis*; surface fibril protein; HSP; diagnosis;  
 KW infection; treatment; prevent; antibacterial drug.  
 XX *Neisseria meningitidis*.  
 XX Key Location/Qualifiers  
 FT Misc-difference 90 /note= "Encoded by AAT"  
 FT Misc-difference 92 /note= "Encoded by GAT"  
 FT Misc-difference 98 /note= "Encoded by AAC"  
 FT Misc-difference 108 /note= "Encoded by AATC"  
 FT Misc-difference 123 /note= "Encoded by ACA"  
 FT Misc-difference 269 /note= "Encoded by AAA"  
 FT Misc-difference 389 /note= "Encoded by CGT"  
 XX WO9958683-A2.  
 XX 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-EP03255.  
 XX 13-MAY-1998; 98GB-0010276.  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Ruelle J;  
 XX WPI; 2000-053103/04.  
 XX N-PSDB; AAZ39865.  
 XX New polypeptide from *Neisseria meningitidis* useful for diagnosis,  
 PT treatment or prevention of bacterial infections in mammal -  
 XX Claim 4; Fig 2; 74pp; English.  
 XX This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
 CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
 CC *Haemophilus influenzae* surface fibril (HSF) protein. The invention  
 CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
 CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
 CC *meningitidis* infection in a mammal. Compositions containing a *Neisseria*  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with *Neisseria*  
 CC *meningitidis* disease. The polynucleotide is useful in the diagnosis of  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes.  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.  
 XX Sequence 591 AA;  
 SQ  
 XX Query Match 99.3%; Score 2981; DB 21; Length 591;  
 XX Best Local Similarity 99.2%; Pred. No. 2.3e-170;  
 XX Matches 586; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLPATVQASANNEOEEDL 60  
 DB 1 mnkiyriiwnlsalnawvavseltrnhtkrasatvktavlatllifatqasanneegee 60  
 QY 61 YLDPVORTVAVLIIVNSOKEGTEKEKVEKNSOWAYYFNEKGVLTARETTLKAGDNLKIKQ 120  
 DB 61 yldpvortvavliivnsoketgekekevnsowayyfeekgvltaretlkagdnlikiq 120  
 QY 121 NGTNFTYSLKDLTDLTSVGTETKLSFANGKVNITSDTKGLNPAKETAGTNGDTTVHLN 180  
 DB 121 ngtnftyslkdldtldtsvgtetklsfngknvntsdtkglnpaketagtngdttvhl 180  
 QY 181 GIGSTLTDPLNLTGATTNVTNDVDDKKRAASVKDVLNAGWNITGVKPGTTASDNVDF 240  
 DB 181 gigstltdplnltgattnvtndvddkkraasvkdvlnagwnitgvpkgttasdnvdf 240  
 QY 241 VRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKLVTKGKKGNGSS 300  
 DB 241 vrtydteflsadtktttnnveskdngkrtevkigaktsvikekdglvtgkdkngas 300  
 QY 301 TDEGEGLVTAKEVIDAVNKAGWRMKTATTANGOTGOADRFETVTSNTVTFASGKTATV 360  
 DB 301 tdegeglvtakevidavnkagwrmtttangotgoadrfetvtsntvtfasgkgtatv 360  
 QY 361 SKDDOGNITVMYDVNVGDALNVQNLNSGWNILDSKAVAGSSGKVTSGNVSPSKGMDV 420  
 DB 361 skddognitvmymydvngdnlvnqnlsgwnilskavagssgkvtsngvpskgmdetv 420  
 QY 421 NINAGNNIETRNKKNIDTATSMTPPOFSSVSLGAGADAPTLSVDGDLNVGSKKDNKPVR 480  
 DB 421 ninagnnietrnknidiatstmpofssvslgagadaptsvdgdlnvgskkdnkpvr 480  
 QY 481 ITNVAPGVKEGDTNVNQLKGVQNLNNDVNDGNARAGIAQAIAATAGLVQAYLPCKSM 540  
 DB 481 itnvapgvkegdtnvnaqlkgvaqnlndvndgnaraglaqalaglvqaylpcksm 540  
 QY 541 MAIGGTYRGEAGYAIYSSISDGGNWIITKTASGNSRGHFASASVGYQM 591  
 DB 541 maiggytyrgeagyaigyssisdggnwiitktasgnsrghfgasasvgyqm 591

RESULT 5  
 AAY23741  
 ID AAY23741 standard; Protein; 591 AA.  
 XX AC AAY23741;  
 XX DT 08-SEP-1999 (first entry)  
 XX DE A surface protein of *Neisseria meningitidis*.  
 XX KW Surface protein; surface glycoprotein; infection; vaccine;  
 XX immunoreactive peptide.  
 XX OS *Neisseria meningitidis*.  
 XX PN WO9931132-A1.  
 XX PD 24-JUN-1999.  
 XX PF 14-DEC-1998; 98WO-AU01031.  
 XX PR 12-DEC-1997; 97GB-0026398.  
 XX PA (ISIS-) ISIS INNOVATION LTD.  
 XX PA (UYQU ) UNIV QUEENSLAND.  
 XX PI Jennings MP, Moxon ER, Peak IRA;  
 XX WPI; 1999-418754/35.  
 XX DR N-PSDB; AAX85793.  
 XX



PT	Neisseria meningitidis surface proteins useful for treating N. meningitidis infections	
XX	Claim 1; Page 104-106; 132pp; English.	
XX	The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans.	
CC	The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.	
XX	Sequence 591 AA;	
50		
Query Match 99.2%; Score 2980; DB 20; Length 591;		
Best Local Similarity 99.3%; Pred. No. 2.6e-170;		
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;		
Qy	1 MNKYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLLPATVQASANNEEQEDL 60	
Db	1 mnelirliwnsalnawvsvseltrnhtkrasatvktavlatllfatvgasanneeqeedi 60	
Qy	61 YLDPVORTVAVLIIVNSDKEGTGEKVEKVEKVEKVEKVEKVEKVEKVEKVEKVEK 120	
Db	61 yldpvlrtvavliivnsdkegkvekvekvekvekvekvekvekvekvekvek 120	
Qy	121 NGTNYTSLKDLTDLTSVGTGTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180	
Db	121 ngntfyslkkdltdltsvgtgteklsfsangknvitsdtkglnfaketagntgdttvhl 180	
Qy	181 GIGSTLTDLTNTGATNTVNDVTDDEKRAASVKVDVNLNAGWNKGVKPGTTASDNVDF 240	
Db	181 gigestltdlntgattntvndvtddekraasvkvdvnlagnwnkvgkpgttasdnvdf 240	
Qy	241 VRTYDTVEFLSADRTTNTVNESDKNGKTEVKIGAKTSVIEKDGKLVTKGDKGENSS 300	
Db	241 vrttdtveflsadtntvnesdkngktevkiaktsviekdgklvtkgdkgengss 300	
Qy	301 TDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTGOADRFETVTSGTNTVTFASGKGTATV 360	
Db	301 tdegeglvtakevidavnkagrmktttangqtgoadrfetvsgtntvtfasgkgtatv 360	
Qy	361 SKDDGNTVTVYDYNVNGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKMDET 420	
Db	361 skddgntvtnvnydvngdlnvnlqnsqwnldkavagssgkvisgnvspskgmdetv 420	
Qy	421 NINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDKNKPVR 480	
Db	421 ninagnnieitrnknidiatstmpqfssvslgagadaptilsvdgdalnvsgskdknkpvr 480	
Qy	481 ITNVAPVKEGDVTVNAQKGVQAQNNRDNVDGNRAGIAQAATATAGLQAYLPKSKM 540	
Db	481 itnvapvkegdvtnvaqkgvagnlnrldnvdgnragiaqaataglvaylpqskm 540	
Qy	541 MAIGGTVRGAGVAGVYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591	
Db	541 maiggtyrgeagvaygyssisdggnwiikgtasgnsrghfgasasvgyqw 591	
RESULT 6		
AAU06175	AAU06175 standard; Protein; 591 AA.	
XX	AAU06175;	
AC	24-OCT-2001 (first entry)	
XX	N. meningitidis EG329 surface antigen Nhha polypeptide sequence.	
DE		
XX		

KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine.	
XX	Neisseria meningitidis strain EG329.	
OS	Location/Qualifiers	
XX	Key	
FT	Region	1..50
FT	Region	/label= C1
FT	Region	/note= "Conserved region 1"
FT	Region	51..108
FT	Region	/label= V1
FT	Region	/note= "Variable region 1"
FT	Region	109..120
FT	Region	/label= C2
FT	Region	/note= "Conserved region 2"
FT	Region	121..124
FT	Region	/label= V2
FT	Region	/note= "Variable region 2"
FT	Region	125..188
FT	Region	/label= C3
FT	Region	/note= "Conserved region 3"
FT	Region	189..210
FT	Region	/label= V3
FT	Region	/note= "Variable region 3"
FT	Region	211..229
FT	Region	/label= C4
FT	Region	/note= "Conserved region 4"
FT	Region	230..236
FT	Region	/label= V4
FT	Region	/note= "Variable region 4"
FT	Region	237..251
FT	Region	/label= C5
FT	Region	/note= "Conserved region 5"
XX	WO200155182-A1.	
XX	02-AUG-2001.	
XX	25-JAN-2001; 2001WO-AU00069.	
XX	25-JAN-2000; 2000US-0177917.	
XX	(UYQU ) UNIV QUEENSLAND.	
XX	Peak IRA, Jennings MP;	
XX	WPI; 2001-488774/53.	
XX	N-PSDB; AAS09165.	
XX	New Nhha surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -	
XX	Claim 9; Fig 1; 9lpp; English.	
XX	The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.	
XX	The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.	
XX	Sequence 591 AA;	
50		

```
Best Local Similarity 99.3%; Pred. No. 2,6e-170;
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVAVLATLFPATVQASANNEBQEDL 60
Db 1 mneilrliwosalnawvvseltrnhtkrasatvavlatlfpatvqasanneeqedl 60
QY 61 YLDPVORTVAVLIWNSDKEGTGEKEVEENSDMAVYFNEKGLVLTAREITLKAGDNLKIK 120
Db 61 yldpvlrtvavliwnsdkegtgekeveensdwavfynekgvlvtareitlkagdnlikq 120
QY 121 NGTNTFYSLLKDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
Db 121 ngntntfysllkdltslsvgteklfsaangknvniitstdkglnfaketagtngdttvhl 180
QY 181 GIGSTLTDTLLTGATTNNVNDVTDDEKKRAASVKDVLNAGWNIKGVPKGTTFASDNVDF 240
Db 181 gigstltdtlltgettntvndvtddekkraasvkdvlagnwngkvpkgtttasdnvdf 240
QY 241 VRTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVLEKDGKLVTKDKGNGSS 300
Db 241 vrtydteflsadtktttvnveskdngkktevkiaktsvlekdgklvtgdkngss 300
QY 301 TDEGEGLYTAKEVIDAVNKAQWRMKTTFANGOTGQADKFETVTSCTNVTTFASGKGTATV 360
Db 301 tdegeglytakevidavnkagwrmttfangotgqadkfetvtsctnvttfasgkgtatv 360
QY 361 SKDDOGNITVMYDVNVDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMDFTV 420
Db 361 skddognitvmvdyvndvalnvnglqnsqwnldskavagsgkvisgnvspskgmdetv 420
QY 421 NNAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGALNVGSKKDNKPV 480
Db 421 nnagnnieitrngknidiatsmtptqfssvslgagadapltlsvdgaldnvsgkkdnkpv 480
QY 481 ITNVPAGVKEGDVNTVAQLKGVAQNLNNRIDNVGNARAGIAQAIATAGLVQAYLPKSM 540
Db 481 itnvapgvegdvntvaqlkgvaqnlnnridnvgnaragiataiataglvqaylpkasm 540
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKGTASGNSRGHFGASASVGYQW 591
Db 541 maigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 591

RESULT 7
AY23737
XX AC AY23737;
XX DT 08-SEP-1999 (first entry)
XX DE A surface protein of Neisseria meningitidis.
XX KW Surface protein; surface glycoprotein; infection; vaccine;
XX OS immunoreactive peptide.
XX PN Neisseria meningitidis.
XX PD W09931132-A1.
XX PE 24-JUN-1999.
XX PF 14-DEC-1998; 98WO-AU01031.
XX PR 12-DEC-1997; 97GB-0026398.
XX PA (ISIS-) ISIS INNOVATION LTD.
XX PI (UYQU ) UNIV QUEENSLAND.
XX PI Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
XX DR
```

```
DR N-PSDB; AAX85788.
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX Claim 1; Page 86-87; 132pp; English.
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX Sequence 592 AA;
SQ
Query Match 98.8%; Score 2967.5; DB 20; Length 592;
Best Local Similarity 98.8%; Pred. No. 1.4e-169;
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVAVLATLFPATVQASANNEB-QBED 59
Db 1 mnklyriiwsalnawvvseltrnhtkrasatvavlatlfpatvqasannerprkdd 60
QY 60 YLDPVORTVAVLIWNSDKEGTGEKEVEENSDMAVYFNEKGLVLTAREITLKAGDNLKIK 119
Db 61 yldpvlrtvavliwnsdkegtgekeveensdwavfynekgvlvtareitlkagdnlik 120
QY 120 QNGTNTFYSLLKDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHL 179
Db 121 qngntntfysllkdltslsvgteklfsaangknvniitstdkglnfaketagtngdttvhl 180
QY 180 NGIGSTLTDTLLTGATTNNVNDVTDDEKKRAASVKDVLNAGWNIKGVPKGTTFASDNVD 239
Db 181 ngigstltdtlltgettntvndvtddekkraasvkdvlagnwngkvpkgtttasdnvd 240
QY 240 FVRTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVLEKDGKLVTKDKGNGSS 299
Db 241 fvrtydteflsadtktttvnveskdngkktevkiaktsvlekdgklvtgdkngss 300
QY 300 STDEGEGLYTAKEVIDAVNKAQWRMKTTFANGOTGQADKFETVTSCTNVTTFASGKGTAT 359
Db 301 stdegeglytakevidavnkagwrmttfangotgqadkfetvtsctnvttfasgkgtat 360
QY 360 VSKDDOGNITVMYDVNVDALNVNQLNSGWNLDKSAVAGSGKVISGNVSPSKGMDFT 419
Db 361 vskddognitvmvdyvndvalnvnglqnsqwnldskavagsgkvisgnvspskgmdet 420
QY 420 VNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGALNVGSKKDNKPV 479
Db 421 vninagnnieitrngknidiatsmtptqfssvslgagadapltlsvdgaldnvsgkkdnkpv 480
QY 480 RITNVPAGVKEGDVNTVAQLKGVAQNLNNRIDNVGNARAGIAQAIATAGLVQAYLPKGS 539
Db 481 ritnvapgvegdvntvaqlkgvaqnlnnridnvgnaragiataiataglvqaylpkgs 540
QY 540 MMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKGTASGNSRGHFGASASVGYQW 591
Db 541 mmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 592

RESULT 8
AY23740
XX ID AY23740 standard; Protein; 594 AA.
XX AC AY23740;
XX DT 08-SEP-1999 (first entry)
XX DR
```

55/ gttatvskdqqgnltvmydvnnvgdaahvnqiqnsgwnlaskavagssgkvisgnvpskg 410

```

SQ Sequence 594 AA:
Query Match 92.0%; Score 2762.5; DB 21; Length 594;
Best Local Similarity 92.5%; Pred. No. 2.6e-157;
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLTLFATVQASANNNEDEEDL 60
DB 1 mnkiyriiwsalnawavseltrnhtkrasatvatavlatlilfatvgastdd--dddl 57

QY 61 YLDPVQRTAVVLIVNSDKEGTGEKEKVENSDWAYFNEKGVLTAREITLKAGDNLIKQ 120
DB 58 ylepvqrtavvlisfrsdektgeke-vtedsnwgyfdkkgvltagtitikagdnlikq 116

QY 121 -----NGTFTYSLKRDLTDTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGD 174
DB 117 ntentnassfyslkkdtdttsvgteklsfsansknvnitsdtkglnfakktatngd 176

QY 175 TTVHLNGIGSTLTDTLLNGATNTVNDVDDKRAASVKDVLNAGWNIGVKPGTTA 234
DB 177 ttvhlngigstltdtllntgatntvndvddkkrasvkdvlngagwnikgvpqgta 236

QY 235 SDNVDFVRTYDFEFLSADTKTTTVNVVESKDNGKTEVKIGAKTSVIKEXDGLVTKDK 294
DB 237 sdnvdfvrtvdfeflsadtktttvnveskdngkrtvkegkigaktsvikegdklvtgdk 296

QY 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSNTVFASGK 354
DB 297 gendstdekglvtakevidavnnkagwrmttttangqgtgqadkfetvtsntvtfasgk 356

QY 355 GTTATVSKDQGNITVMYDVNVGDALNVQLNSGWNLDKSAVAGSSGKVISGNVSPSKG 414
DB 357 gttatvskdqgnitvmvdydvngdalnvqlnsgwvnlksavagssgkvisgnvpskg 416

QY 415 KMDFTVNTNAGNIEITRNKGNIDTATMTPOFSSVSLGAGADAPTLSVDGD-ALANVSGK 473
DB 417 kmdeftvntnagnieitrnkgnidatmtpfssvslgagadaptslsvdgdalnvsgk 476

QY 474 KDKKPVRTNVAPGVKEGDTNVNOLKGVQAOINLRIDVNGNARAGIAQATAGLVOA 533
DB 477 dankpvrtnvapgvkegdtvnnolkgvqaoilnrldvngnaragiataqlvga 536

QY 534 YLPKSMMAIGGTYRGEAGYAGYISISDGGNWIKGTASGNSGRHFGASASVGYQW 591
DB 537 ylpksmmaiggyrgeagyaigyssisdggnwiikgtasgnsgnrhfgasasvgyqw 594

RESULT 10
AAU06174
XX AAU06174 standard; Protein: 594 AA.
XX AAU06174;
XX 24-OCT-2001 (first entry)
XX N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain EG327.
XX Key Location/Qualifiers
XX Region 1..50 /label= C1
XX /note= "Conserved region 1"
XX Region 51..104 /label= V1
XX /note= "Variable region 1"
XX Region 105..116 /label= C2
XX /note= "Conserved region 2"
XX Region 117..126

/label= V2
/note= "Variable region 2"
127..190
/label= C3
/note= "Conserved region 3"
191..212
/label= V3
/note= "Variable region 3"
213..231
/label= C4
/note= "Conserved region 4"
232..238
/label= V4
/note= "Variable region 4"
239..294
/label= C5
/note= "Conserved region 5"

WO200155182-A1.
02-AUG-2001.
25-JAN-2001; 2001WO-AU00069.
25-JAN-2000; 2000US-0177917.
(UYQU ) UNIV QUEENSLAND.
Peak IRA, Jennings MP;
WPI: 2001-488774/53.
N-PSDB; AAS09164.
New NhhA surface antigen polypeptides and polynucleotides from
Neisseria meningitidis, useful in producing vaccines for treating or
preventing broad spectrum of Neisseria meningitidis -
Claim 9; Fig 1; 91pp; English.
The present invention relates to the isolation of novel Neisseria
meningitidis mutant polypeptides of the surface antigen NhhA
(AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
characterised by deletions of non-conserved amino acids, particularly
the deletion of variable regions. The deletion mutants are useful in
diagnostics, therapeutic and prophylactic vaccines against a broader
spectrum of N. meningitidis, and in designing and/or screening of
medicaments. The mutant proteins when used as a vaccine can effectively
immunise against a broader spectrum of N. meningitidis strains than
would be expected from a corresponding wild-type surface antigen.
The present sequence representing the wild type surface antigen NhhA
from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences
(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
the present invention.
Sequence 594 AA;

Query Match 92.0%; Score 2762.5; DB 22; Length 594;
Best Local Similarity 92.5%; Pred. No. 2.6e-157;
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLTLFATVQASANNNEDEEDL 60
DB 1 mnkiyriiwsalnawavseltrnhtkrasatvatavlatlilfatvgastdd--dddl 57

QY 61 YLDPVQRTAVVLIVNSDKEGTGEKEKVENSDWAYFNEKGVLTAREITLKAGDNLIKQ 120
DB 58 ylepvqrtavvlisfrsdektgeke-vtedsnwgyfdkkgvltagtitikagdnlikq 116

QY 121 -----NGTFTYSLKRDLTDTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGD 174
DB 117 ntentnassfyslkkdtdttsvgteklsfsansknvnitsdtkglnfakktatngd 176

```

```
Oy 175 TTVHLNGIGSTLTDFLLNTGATTNTVNDVTDDEKKRAASVKVDVLNAGWNIGKVGKPGTTA 234
Db 177 tcvhnglsgstltdtllntgattntvndvtddekkraasvkdvlntagwnlkgvkpgtta 236

Oy 235 SDNVDFVRTYDTVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVKEKDGKLVTKGDK 294
Db 237 sdnvdfvrttydtveflsadtktttvnveskngkrtvkvigaktsvikekgklvtgdk 296

Oy 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKPEFTVTSNTVTFASGK 354
Db 297 gendstdekgeglvtakevidavnkagwrmttttangotgqadkfetvtsntvtfasgk 356

Oy 355 GTTATVSKDDOGNITVMYDVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
Db 357 gttatvskddognitvmymydvngdlnvnqlnsgwnldskavagssgkvisgnvpskg 416

Oy 415 KMDETVMNAGNIIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
Db 417 kmdevmnagnnleitrngknidiatsmtpqfssvslgagadaptlsvdddegalnvsgk 476

Oy 474 KDNKPVRTNVPAGVKEGDTVNVQALKGVAQNLRNIDVGNARAGIAQAATATAGLVQA 533
Db 477 dankpvrtnvpagvkegdvtnvaqlkgvaqnlrnhidvgnaragiaqaiaataglvqa 536

Oy 534 YLPKGSMAIAGGTVRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591
Db 537 ylpkgsmaiaaggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594
```

## RESULT 11

```
AAU06179
ID AAU06179 standard; Protein: 594 AA.
```

```
AC AAU06179;
```

```
DT 08-SEP-1999 (first entry)
```

```
DE A surface protein of Neisseria meningitidis.
```

```
EW Surface protein: surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
```

```
XX Neisseria meningitidis.
```

```
OS WO9931132-A1.
```

```
PN 24-JUN-1999.
```

```
PD 14-DEC-1998; 98WO-AU01031.
```

```
PR 12-DEC-1997; 97GB-0026398.
```

```
XX (ISIS-) ISIS INNOVATION LTD.
```

```
PA (UYOU) UNIV QUEENSLAND.
```

```
XX Jennings MP, Moxon ER, Peak IRA;
```

```
XX WPI; 1999-418754/35.
```

```
DR N-PSDB; AAX85791.
```

```
XX Neisseria meningitidis surface proteins useful for treating N.
```

```
PT meningitidis infections
```

```
XX Claim 1; Page 95-97; 132pp; English.
```

```
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
```

```
CC be used to identify immunoreactive peptides.
```

```
XX Sequence 594 AA;
```

```
Query Match 91.1%; Score 2736.5; DB 20; Length 594;
Best Local Similarity 92.0%; Pred. No. 9.4e-156;
Matches 550; Conservative 11; Mismatches 26; Indels 11; Gaps 4;
```

```
Oy 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASANNEQEEEDL 60
Db 1 mnkiyriiwnsalnawvseltrnhtrkasatvatavtatlflfatvqanad---dddl 57
```

```
Oy 61 YLDPVQRTVAVILIVNSDKEGTEKEKVEESDMAYVFNKGLVTAIREITLKAGDNLKIK 120
Db 58 ylepvqrtavvlisfrskdtegekted-snvayvfdekrvlkagaitlkagdnlikq 116
```

```
Oy 121 -----NGTNFTYSUKKDLTDLTTSVGTETKLSFANGKNVITSYDTKGLNFAKETAGTNGD 174
Db 117 ntentndssftysikkdltdltsveteklsfngangknvitsdtkglnfaketagngd 176
```

```
Oy 175 TTVHLNGIGSTLTDFLLNTGATTNTVNDVTDDEKKRAASVKVDVLNAGWNIGKVGKPGTTA 234
Db 177 tcvhnglsgstltdtllntgattntvndvtddekkraasvkdvlntagwnlkgvkpgtta 236
```

```
Oy 235 SDNVDFVRTYDTVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVKEKDGKLVTKGDK 294
Db 237 sdnvdfvrttydtveflsadtktttvnveskngkrtvkvigaktsvikekgklvtgdk 296
```

```
Oy 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKPEFTVTSNTVTFASGK 354
Db 297 gendstdekgeglvtakevidavnkagwrmttttangotgqadkfetvtsntvtfasgk 356
```

```
Oy 355 GTTATVSKDDOGNITVMYDVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
Db 357 gttatvskddognitvmymydvngdlnvnqlnsgwnldskavagssgkvisgnvpskg 416
```

```
Oy 415 KMDETVMNAGNIIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
Db 417 kmdevmnagnnleitrngknidiatsmtpqfssvslgagadaptlsvdddegalnvsgk 476
```

```
Oy 474 KDNKPVRTNVPAGVKEGDTVNVQALKGVAQNLRNIDVGNARAGIAQAATATAGLVQA 533
Db 477 dankpvrtnvpagvkegdvtnvaqlkgvaqnlrnhidvgnaragiaqaiaataglvqa 536
```

```
Oy 534 YLPKGSMAIAGGTVRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591
Db 537 ylpkgsmaiaaggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594
```

## RESULT 12

```
AAU06179
ID AAU06179 standard; Protein: 594 AA.
```

```
AC AAU06179;
```

```
DT 24-OCT-2001 (first entry)
```

```
XX N. meningitidis BZ198 surface antigen NHA surface antigen NHA polypeptide sequence.
```

```
DE Surface antigen NHA; meningococcal disease; meningitis vaccine.
```

```
XX Neisseria meningitidis strain BZ198.
```

```
XX Key Location/Qualifiers
```

```
FT Region 1..50
```

```
FT /label= C1
```

```
FT /note= "Conserved region 1"
```

```
FT Region 51..104
```

```
FT /label= V1
```

```
FT /note= "variable region 1"
```

```
FT Region 105..116
```

```
FT /label= C2
```



```
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 90.6%; Score 2721.5; DB 20; Length 598;
Best Local Similarity 90.9%; Pred. No. 7.5e-155;
Matches 547; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

Qy 1 MNKYRIIWNALNANWAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60
Db 1 mnkyriiwnsalnawvseltrnhktrasatvatavlatllfatvganatd---dddl 57
Qy 61 YLDPQRTAVLIVNSDKGEKGEKVEENSDWAVYNEKGVLTAREITLKAGDNLIKQ 120
Db 58 ylepvqrtavvlvsfrsdegkegked-snwavyfdekrvlkagaitlkagdnlikq 116
Qy 121 -----NGTNYTSLKRDLDLTLSVGTPEKLSFGSANGKNVITSDTKGLNFAKETAG 170
Db 117 ntntentntdsftyslkkldltsveteklsfgangknvitsdtkglnfaketag 176
Qy 171 TNGOTTVHLNGIGSTLDTLNTGATNTVNDVNTDDEKKRAASVKOVNAGWNIKGVKP 230
Db 177 tngdptvhlngigstltdlntgattntvndvntddekrraasvkdvlnagwnlkgvqp 236
Qy 231 GTTASDNVDFVRTYDTVEFLSADTKTTVNVESKDNCKKTEVKIGAKTSVLEKDGKLV 290
Db 237 gttasdnvdfvrtvdtveflsadtkttvnveskdngkktevkigaktsvlekdgklvt 296
Qy 291 GKDRGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGAQDKFETVTSQTNVTF 350
Db 297 gkgdengsstdegeglvtakevidavnkagwrnktttangtqtgqadkfetvsgtkvtf 356
Qy 351 ASRGKTATVSKDDOQNTVYDWNVDALNVQNSGWNLDKSAVAGSGKVISGNVS 410
Db 357 asrgktatvskddqgnltvkvdyvvnvgdalinvnqlqnsqwnldskavagsgkvisgnvs 416
Qy 411 PSKGMDETVNINAGNTEITRNKNTDIATSMTPQSSVSLGACADAPTLSDGCD-ALN 469
Db 417 pskqmetvningnlnlelcrngkndia tsmtpqfssvslgagadaptlsvddegain 476
Qy 470 VGSKKDNKPVRTITVAPGVKEGDVTNVLAQLKGAQNLNRRIDNVDGNARAGIAQAIATAG 529
Db 477 vgsdkdnkpvritnvapgvkegvtvnaqlkgvaqnlrridnvdgnaragiaqaiatag 536
Qy 530 LVQAYLPCKSMMAIGGGTYRGEAGYAIQYSSISDGGNWIIGKTASGNSRHFASASVGY 589
Db 537 laqaylpqksmmaigggtyrgeagyaigyssidsdgtgnwnviktasgnsrghfgasasvgy 596
Qy 590 QW 591
Db 597 qw 598

RESULT 14
AAU06177
ID AAU06177 standard; Protein; 598 AA.
XX
AC AAU06177;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H15 surface antigen NhhA polypeptide sequence.
XX
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H15.
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
```

```
FT /note= "Conserved region 1"
FT 51..104
FT /label= V1
FT /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..130
FT /label= V2
FT /note= "Variable region 2"
FT 131..194
FT /label= C3
FT /note= "Conserved region 3"
FT 195..216
FT /label= V3
FT /note= "Variable region 3"
FT 217..235
FT /label= C4
FT /note= "Conserved region 4"
FT 236..242
FT /label= V4
FT /note= "Variable region 4"
FT 243..598
FT /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
WPI: 2001-488774/53.
N-PSDB: AAS09167.
XX
New NhhA surface antigen polypeptides and polynucleotides from
Neisseria meningitidis, useful in producing vaccines for treating or
preventing broad spectrum of Neisseria meningitidis .
XX
Claim 9; Fig 1; 91pp; English.
XX
The present invention relates to the isolation of novel Neisseria
meningitidis mutant polypeptides of the surface antigen NhhA
(AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
characterised by deletions of non-conserved amino acids, particularly
the deletion of variable regions. The deletion mutants are useful in
diagnostics, therapeutic and prophylactic vaccines against a broader
spectrum of N. meningitidis, and in designing and/or screening of
medicaments. The mutant proteins when used as a vaccine can effectively
immunise against a broader spectrum of N. meningitidis strains than
would be expected from a corresponding wild-type surface antigen.
XX
The present sequence representing the wild type surface antigen NhhA
from N. meningitidis strain H15 is 1 of 10 NhhA polypeptide sequences
(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
the present invention.
XX
SQ Sequence 598 AA;
```

```
Query Match 90.6%; Score 2721.5; DB 22; Length 598;
Best Local Similarity 90.9%; Pred. No. 7.5e-155;
Matches 547; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

Qy 1 MNKYRIIWNALNANWAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60
Db 1 mnkyriiwnsalnawvseltrnhktrasatvatavlatllfatvganatd---dddl 57
```

```
QY 61 YLDPVORTVAVLIIVNSDKGEGEKEKVEENSDWAVYFNPKGVLTAREITLTKAGDNLKIKQ 120
DB 58 YLEPVRTAVVLSFRSDKEGEGEGEGEDT-snwavyfdekrvlkagaitlkagdnkikq 116
QY 121 -----NGTNFTYSLKKDLPLDFTSVGTEKLSFANGKNVNITSDTKGLNFAKETAG 170
DB 117 ntntentndssftyslkkdllditsveteklsfgangknvnitsdtkglnfaketag 176
QY 171 TNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKIGVKP 230
DB 177 tngdptvhlngigstltdtllntgattntndvndddekkaasvkdvlmagwnikgvkp 236
QY 231 GTTASDNVDVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVYKEKDKLVT 290
DB 237 gttasdnvdfvrytdtveflsadtktttvnveskdngkktvkvigaktsvikekdglvt 296
QY 291 GKDKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTMTTANGOTGOADKFEVTSCTNVTF 350
DB 297 gkgkdngsstdegeglvtakevidavnkagwrmtktttangotgogadkfevtsgtkvtf 356
QY 351 ASGKGTATVSKDDGNGITVMYDVNVDGDLNVNQLNSGWNLDKAVAGSGKVISGNVS 410
DB 357 asngtatacvskddgngitvmydvnvvgdalnvnqldnsqwnldskavagsgkvisgnvs 416
QY 411 PSKGKMDFTVNIAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-ALN 469
DB 417 pskgkmdetvniagnnieitrngknidiatsmtppqfssvslgagadaptlsvdddegaln 476
QY 470 VGSKDKNKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATATAG 529
DB 477 vgskdankpvrntnvapgvkegdtnvaqlkgvaqnlrnidnvgnaragiaqaiaatag 536
QY 530 LVQAYLPKSKMMAIGGGPYRGEAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGY 589
DB 537 laqaylpkksmmaigggpyrgeagayagysissdgnwiiikgtasgnsrhfgasasvgy 596
QY 590 QW 591
DB 597 qw 598

RESULT 15
AAI23738 standard; Protein; 598 AA.
ID AAI23738;
AC AAY23738;
DT 08-SEP-1999 (first entry)
DE A surface protein of Neisseria meningitidis.
KW Surface protein; surface glycoprotein; infection; vaccine;
KW Immunoreactive peptide.
OS Neisseria meningitidis.
PN W09931132-A1.
PD 24-JUN-1999.
PF 14-DEC-1998; 98WO-AU01031.
PR 12-DEC-1997; 97GB-0026398.
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
XX N-PSDB; AAX85790.
XX Neisseria meningitidis surface proteins useful for treating N.
PT
```

```
PT meningitidis infections
XX Claim 1; Page 91-93; 132pp; English.
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX Sequence 598 AA;
SQ
```

```
Query Match 90.3%; Score 2712.5; DB 20; Length 598;
Best local similarity 90.5%; Pred. No. 2.6e-154;
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;
QY 1 MNKYRIIWSALNAWVASELTRNHTKRASATVKTAVLATLFPATVQASANNEOEEDL 60
DB 1 mnkysriiwsalnawvaseltrnhtkrasatvatavlatlfpatvqanatl---dddl 57
QY 61 YLDPVORTVAVLIIVNSDKGEGEKEKVEENSDWAVYFNPKGVLTAREITLTKAGDNLKIKQ 120
DB 58 YLEPVRTAVVLSFRSDKEGEGEGEDT-snwavyfdekrvlkagaitlkagdnkikq 116
QY 121 -----NGTNFTYSLKKDLDTLTSVTEKLSFANGKNVNITSDTKGLNFAKETAG 170
DB 117 ntntentndssftyslkkdllditsveteklsfgangknvnitsdtkglnfaketag 176
QY 171 TNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKIGVKP 230
DB 177 tngdptvhlngigstltdtllntgattntndvndddekkaasvkdvlmagwnikgvkp 236
QY 231 GTTASDNVDVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVYKEKDKLVT 290
DB 237 gttasdnvdfvrytdtveflsadtktttvnveskdngkrtvkvigaktsvikekdglvt 296
QY 291 GKDKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTMTTANGOTGOADKFEVTSCTNVTF 350
DB 297 gkgkdngsstdegeglvtakevidavnkagwrmtktttangotgogadkfevtsgtkvtf 356
QY 351 ASGKGTATVSKDDGNGITVMYDVNVDGDLNVNQLNSGWNLDKAVAGSGKVISGNVS 410
DB 357 asngtatacvskddgngitvmydvnvvgdalnvnqldnsqwnldskavagsgkvisgnvs 416
QY 411 PSKGKMDFTVNIAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-ALN 469
DB 417 pskgkmdetvniagnnieitrngknidiatsmtppqfssvslgagadaptlsvdddegaln 476
QY 470 VGSKDKNKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATATAG 529
DB 477 vgskdankpvrntnvapgvkegdtnvaqlkgvaqnlrnidnvgnaragiaqaiaatag 536
QY 530 LVQAYLPKSKMMAIGGGPYRGEAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGY 589
DB 537 laqaylpkksmmaigggpyrgeagayagysissdgnwiiikgtasgnsrhfgasasvgy 596
QY 590 QW 591
DB 597 qw 598
```

Search completed: September 5, 2002, 10:23:16  
Job time: 478 sec





**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:46 : Search time 25.63 seconds  
(without alignments)  
563.228 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGSRGHFGASVGYOW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pap.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pap.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pap.\*  
5: /cgn2\_6/ptodata/2/iaa/PT05\_COMB.pap.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2999	99.9	591	US-09-377-155-21	Sequence 21, Appl
2	2999	99.9	591	US-09-669-974-21	Sequence 21, Appl
3	2980	99.2	591	US-09-377-155-11	Sequence 11, Appl
4	2980	99.2	591	US-09-669-974-11	Sequence 11, Appl
5	2967.5	98.8	592	US-09-377-155-2	Sequence 2, Appl
6	2967.5	98.8	592	US-09-669-974-2	Sequence 2, Appl
7	2762.5	92.0	594	US-09-377-155-9	Sequence 9, Appl
8	2762.5	92.0	594	US-09-669-974-9	Sequence 9, Appl
9	2736.5	91.1	594	US-09-377-155-7	Sequence 7, Appl
10	2736.5	91.1	594	US-09-669-974-7	Sequence 7, Appl
11	2721.5	90.6	598	US-09-377-155-13	Sequence 13, Appl
12	2721.5	90.6	598	US-09-669-974-13	Sequence 13, Appl
13	2712.5	90.3	598	US-09-377-155-5	Sequence 5, Appl
14	2712.5	90.3	598	US-09-669-974-5	Sequence 5, Appl
15	2689	89.5	599	US-09-377-155-15	Sequence 15, Appl
16	2689	89.5	599	US-09-669-974-15	Sequence 15, Appl
17	2577.5	85.8	592	US-09-377-155-17	Sequence 17, Appl
18	2577.5	85.8	592	US-09-669-974-17	Sequence 17, Appl
19	2475	82.4	589	US-09-377-155-19	Sequence 19, Appl
20	2475	82.4	589	US-09-669-974-19	Sequence 19, Appl
21	1245	41.5	2411	US-09-268-347-36	Sequence 36, Appl
22	1243	41.4	2353	US-09-377-155-33	Sequence 33, Appl
23	1243	41.4	2353	US-08-913-942-4	Sequence 4, Appl
24	1243	41.4	2353	US-09-669-974-33	Sequence 33, Appl
25	1242	41.4	2354	US-09-268-347-47	Sequence 47, Appl
26	1180.5	39.3	607	US-08-409-995-6	Sequence 6, Appl
27	1180.5	39.3	607	US-08-685-467-6	Sequence 6, Appl

28	1180.5	39.3	607	4	US-08-913-942-6	Sequence 6, Appl
29	1180.5	39.3	1912	1	US-08-409-995-4	Sequence 4, Appl
30	1180.5	39.3	1912	3	US-08-685-467-4	Sequence 4, Appl
31	1070.5	35.6	1094	4	US-09-268-347-32	Sequence 32, Appl
32	1057.5	35.2	1098	1	US-08-409-995-2	Sequence 2, Appl
33	1057.5	35.2	1098	3	US-08-685-467-2	Sequence 2, Appl
34	1057.5	35.2	1098	4	US-09-377-155-32	Sequence 32, Appl
35	1057.5	35.2	1098	4	US-08-913-942-2	Sequence 2, Appl
36	1057.5	35.2	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1057.5	35.2	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1039.5	34.6	658	1	US-08-409-995-5	Sequence 5, Appl
39	1039.5	34.6	658	3	US-08-685-467-5	Sequence 5, Appl
40	1039.5	34.6	658	4	US-08-913-942-5	Sequence 5, Appl
41	995	33.1	679	4	US-08-913-942-15	Sequence 15, Appl
42	995	33.1	679	4	US-09-268-347-26	Sequence 26, Appl
43	752.5	25.1	1004	4	US-09-268-347-30	Sequence 30, Appl
44	741.5	24.7	1002	4	US-09-268-347-24	Sequence 24, Appl
45	696.5	23.2	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-21  
: Sequence 21, Application US/09377155  
: Patent No. 6197312  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/377,155  
: PRIOR FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB/9726398.2  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: Patentin Ver. 2.0  
: SEQ ID NO 21  
: LENGTH: 591  
: TYPE: PRT  
: ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match	99.9%	Score 2999;	DB 4;	Length 591;
Best Local Similarity	99.8%	Pred. No. 6.7e-225;		
Matches 590;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNNEDEEDL	60	
Db	1	MNKIYRIIWSALNAWVVSSELTRNHTKRASATVKTAVLATLLFATVQASANNNEDEEDL	60	
QY	61	YLDPQVTVAVLIVNSDKGTGKEKEVEENSDWAVFNEKGVLTAREITLKAGDNLKIQ	120	
Db	61	YLDPQVTVAVLIVNSDKGTGKEKEVEENSDWAVFNEKGVLTAREITLKAGDNLKIQ	120	
QY	121	NGTNFTYSLKDLTDLTSVGTGKLSFANGKNVITSDTKGLNFAKETAGTNGDTTTHLN	180	
Db	121	NGTNFTYSLKDLTDLTSVGTGKLSFANGKNVITSDTKGLNFAKETAGTNGDTTTHLN	180	
QY	181	GIGSLTDLTLLNTGATTNTNDVDEKRAASVKDVLNAGWNKGVKPGTTASNDVF	240	
Db	181	GIGSLTDLTLLNTGATTNTNDVDEKRAASVKDVLNAGWNKGVKPGTTASNDVF	240	
QY	241	VRTYDVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIREKDGKLVTKDKGNGSS	300	
Db	241	VRTYDVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIREKDGKLVTKDKGNGSS	300	
QY	301	TDEGGLVTAKEVIDAVNAGRWMTTANGOTGOADKFEVTSGTNTVTFASGKGTATV	360	

|||||  
Db 301 TDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPEFVTSCTNVTFSAGKGTATV 360  
QY 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVIISGNVSPSKGMDVTV 420  
Db 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVIISGNVSPSKGMDVTV 420  
QY 421 NINAGNIEITRNKKNIDTATSMTPQSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
Db 421 NINAGNIEITRNKKNIDTATSMTPQSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
QY 481 ITNAPGVKEGDVTNVAQLKGVAQNLRNIDVGNARAGIAQAATATAGLVQAYLPKSKM 540  
Db 481 ITNAPGVKEGDVTNVAQLKGVAQNLRNIDVGNARAGIAQAATATAGLVQAYLPKSKM 540  
QY 541 MAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYOW 591  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYOW 591

## RESULT 2

US-09-669-974-21  
; Sequence 21; Accession: **U03068974**  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 99.98%; Score 2999; DB 4; Length 591;  
Best Local Similarity 99.88%; Pred No. 6.7e-225;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWSALNANWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
Db 1 MNKIYRIIWSALNANWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
QY 61 YLDPVORTVAVLIIVNSDEKTEGTEKEKEVEENSOWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
Db 61 YLDPVORTVAVLIIVNSDEKTEGTEKEKEVEENSOWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
QY 121 NGNFTYSLKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDITVHLN 180  
Db 121 NGNFTYSLKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDITVHLN 180  
QY 181 GIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
Db 181 GIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
QY 241 VRTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTGKDKGENSS 300  
Db 241 VRTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTGKDKGENSS 300  
QY 301 TDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPEFVTSCTNVTFSAGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPEFVTSCTNVTFSAGKGTATV 360

Db 301 TDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPEFVTSCTNVTFSAGKGTATV 360  
QY 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVIISGNVSPSKGMDVTV 420  
Db 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVIISGNVSPSKGMDVTV 420  
QY 421 NINAGNIEITRNKKNIDTATSMTPQSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
Db 421 NINAGNIEITRNKKNIDTATSMTPQSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
QY 481 ITNAPGVKEGDVTNVAQLKGVAQNLRNIDVGNARAGIAQAATATAGLVQAYLPKSKM 540  
Db 481 ITNAPGVKEGDVTNVAQLKGVAQNLRNIDVGNARAGIAQAATATAGLVQAYLPKSKM 540  
QY 541 MAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYOW 591  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYOW 591

## RESULT 3

US-09-377-155-11  
; Sequence 11; Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 99.2%; Score 2980; DB 4; Length 591;  
Best Local Similarity 99.3%; Pred No. 2e-223;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWSALNANWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
Db 1 MNKIYRIIWSALNANWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
QY 61 YLDPVORTVAVLIIVNSDEKTEGTEKEKEVEENSOWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
Db 61 YLDPVORTVAVLIIVNSDEKTEGTEKEKEVEENSOWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
QY 121 NGNFTYSLKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDITVHLN 180  
Db 121 NGNFTYSLKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDITVHLN 180  
QY 181 GIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
Db 181 GIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
QY 241 VRTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTGKDKGENSS 300  
Db 241 VRTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTGKDKGENSS 300  
QY 301 TDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPEFVTSCTNVTFSAGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPEFVTSCTNVTFSAGKGTATV 360  
QY 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVIISGNVSPSKGMDVTV 420

Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKGKMDTV 420  
Qy 421 NINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLLSVGDALNVGSKDKNKPVR 480  
Db 421 NINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLLSVGDALNVGSKDKNKPVR 480  
Qy 481 ITNVPAGVKEGVDVTNVAQLKGAONLNNRDNVDGNARAGIAQAATATAGLVQAYLPGKSM 540  
Db 481 ITNVPAGVKEGVDVTNVAQLKGAONLNNRDNVDGNARAGIAQAATATAGLVQAYLPGKSM 540  
Qy 541 MAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGHFGASASVGYQW 591

## RESULT 4

US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6,693,373  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 99.28; Score 2980; DB 4; Length 591;  
Best Local Similarity 99.38; Pred. No. 2e-223;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MNKYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEDL 60  
Db 1 MNEILRIIWNALNAWVVSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEDL 60  
Qy 61 YLDPVORTVAVLIIVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAREITLKAGDNLIK 120  
Db 61 YLDPVORTVAVLIIVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAREITLKAGDNLIK 120  
Qy 121 NGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
Qy 181 GIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDF 240  
Db 181 GIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDF 240  
Qy 241 VRTYDTEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTKCKDKGENSS 300  
Db 241 VRTYDTEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTKCKDKGENSS 300  
Qy 301 TDEGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFEITVTSCTNVTFAAGKGTATV 360  
Db 301 TDEGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFEITVTSCTNVTFAAGKGTATV 360  
Qy 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKGKMDTV 420  
Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKGKMDTV 420

Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKGKMDTV 420  
Qy 421 NINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLLSVGDALNVGSKDKNKPVR 480  
Db 421 NINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLLSVGDALNVGSKDKNKPVR 480  
Qy 481 ITNVPAGVKEGVDVTNVAQLKGAONLNNRDNVDGNARAGIAQAATATAGLVQAYLPGKSM 540  
Db 481 ITNVPAGVKEGVDVTNVAQLKGAONLNNRDNVDGNARAGIAQAATATAGLVQAYLPGKSM 540  
Qy 541 MAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGHFGASASVGYQW 591

## RESULT 5

US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6,197,312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 98.88; Score 2967.5; DB 4; Length 592;  
Best Local Similarity 98.88; Pred. No. 1.9e-222;  
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 MNKYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEE-QED 59  
Db 1 MNKYRIIWNALNAWVVSELTRNHTKRASATVKTAVLATLLFATVOASANNRPRKD 60  
Qy 60 YLDPVORTVAVLIIVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAREITLKAGDNLIK 119  
Db 61 YLDPVORTVAVLIIVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAREITLKAGDNLIK 120  
Qy 120 QNGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHL 179  
Db 121 QNGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180  
Qy 180 NGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTASDNVD 239  
Db 181 NGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTASDNVD 240  
Qy 240 FVRTYDTEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTKCKDKGENGS 299  
Db 241 FVRTYDTEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDKGLVTKCKDKGENGS 300  
Qy 300 STDGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFEITVTSCTNVTFAAGKGTAT 359  
Db 301 STDGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFEITVTSCTNVTFAAGKGTAT 360  
Qy 360 VSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKGKMDTV 419  
Db 361 VSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKGKMDTV 420  
Qy 420 VNINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLLSVGDALNVGSKDKNKP 479

Db 421 VNINAGNTEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPV 480  
QY 480 RITNAPGVKEGDTNVAQLKGVAONLNRRIDNVNDRAGIAQAIAATAGLVQAYLPCKS 539  
Db 481 RITNAPGVKEGDTNVAQLKGVAONLNRRIDNVNDRAGIAQAIAATAGLVQAYLPCKS 540  
QY 540 MMAIGGTYRGAGYAGYSSISDGGNWIILKTASGNSRGHFGASASVGYOW 591  
Db 541 MMAIGGTYRGAGYAGYSSISDGGNWIILKTASGNSRGHFGASASVGYOW 592

RESULT 6  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 98.8%; Score 2967.5; DB 4; Length 592;  
Best Local Similarity 98.8%; Pred. No. 1.9e-222;  
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNPE-OED 59  
Db 1 MNKIYRIWNSALNAWVSELTRNHTKRASATVKTAVLATLLFATVQASANNRPKKD 60  
QY 60 LYLDPVORTVAVLIIVNSDKETGEGEKEVEENSDWAVYFNEKGVLTAREITLLKAGDNLKIK 119  
Db 61 LYLDPVORTVAVLIIVNSDKETGEGEKEVEENSDWAVYFNEKGVLTAREITLLKAGDNLKIK 120  
QY 120 QNGTFTYSLKKDLTDLTSVGTCKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 179  
Db 121 QNGTFTYSLKKDLTDLTSVGTCKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 180  
QY 180 NGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASNDVD 239  
Db 181 NGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASNDVD 240  
QY 240 FVRTYDTEFFLSADTKTTTVNVEKDKNGKTEVKGAKTSVTEKDKGLVTKDGKNGS 299  
Db 241 FVRTYDTEFFLSADTKTTTVNVEKDKNGKTEVKGAKTSVTEKDKGLVTKDGKNGS 300  
QY 300 STDDEGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGKGTAT 359  
Db 301 STDDEGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGKGTAT 360  
QY 360 VSKDDQGNITVMYDVNVDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDT 419  
Db 361 VSKDDQGNITVMYDVNVDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDT 420  
QY 420 VNINAGNTEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPV 479

Db 421 VNINAGNTEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPV 480  
QY 480 RITNAPGVKEGDTNVAQLKGVAONLNRRIDNVNDRAGIAQAIAATAGLVQAYLPCKS 539  
Db 481 RITNAPGVKEGDTNVAQLKGVAONLNRRIDNVNDRAGIAQAIAATAGLVQAYLPCKS 540  
QY 540 MMAIGGTYRGAGYAGYSSISDGGNWIILKTASGNSRGHFGASASVGYOW 591  
Db 541 MMAIGGTYRGAGYAGYSSISDGGNWIILKTASGNSRGHFGASASVGYOW 592

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 92.0%; Score 2762.5; DB 4; Length 594;  
Best Local Similarity 92.5%; Pred. No. 1.6e-206;  
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;  
QY 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNPEQEDL 60  
Db 1 MNKIYRIWNSALNAWVSELTRNHTKRASATVKTAVLATLLFATVQASTTD---DDDL 57  
QY 61 LYLDPVORTVAVLIIVNSDKETGEGEKEVEENSDWAVYFNEKGVLTAREITLLKAGDNLKIK 120  
Db 58 LYLDPVORTVAVLIIVNSDKETGEGEKEVEENSDWAVYFNEKGVLTAREITLLKAGDNLKIK 116  
QY 121 -----NGTFTYSLKKDLTDLTSVGTCKLSFSAANGKNVNTSDTKGLNFAKETAGTNGD 174  
Db 117 NTNENTNASSFTYSLKKDLTDLTSVGTCKLSFSAANGKNVNTSDTKGLNFAKETAGTNGD 176  
QY 175 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 234  
Db 177 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
QY 235 SDNVDFVRTYDTEFFLSADTKTTTVNVEKDKNGKTEVKGAKTSVTEKDKGLVTKGDK 294  
Db 237 SDNVDFVRTYDTEFFLSADTKTTTVNVEKDKNGKTEVKGAKTSVTEKDKGLVTKGDK 296  
QY 295 GENGSTDEBGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGK 354  
Db 297 GENGSTDEBGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGK 356  
QY 355 GTTATVSKDDQGNITVMYDVNVDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKG 414  
Db 357 GTTATVSKDDQGNITVMYDVNVDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKG 416  
QY 415 KMDETVNIINAGNTEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSK 473  
Db 417 KMDETVNIINAGNTEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSK 476  
QY 474 KDKPVRTITNAPGVKEGDTNVAQLKGVAONLNRRIDNVNDRAGIAQAIAATAGLVQA 533

Db 477 DANKPVRITNAPVKEGVDVTNVAQLKGVQNLNNHNDVGNARAGIAQAATATAGLVQA 536  
Qy 534 YLPGRSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASASVGYQW 591  
Db 537 YLPGRSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASASVGYQW 594

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 92.0%; Score 2762.5; DB 4; Length 594;  
Best Local Similarity 92.5%; Pred. No. 1.6e-206;  
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;  
Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASANNEQEDL 60  
Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTD---DDDL 57  
Qy 61 YLDPVQRTAVLIVNSDKEGTGEKEKEVEENSDWAYVFNEKGVLTAREITLKAGDNLKIQ 120  
Db 58 YLEPQRTAVLISFSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAITLKAGDNLKIQ 116  
Qy 121 -----NGTNFYSLKKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 174  
Db 117 NTNENTNASFSYSLKKDLTDLTSVTEKLSFSANSKNVNITSDTKGLNFAKKTAEITNGD 176  
Qy 175 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNINIKGVKPGTTA 234  
Db 177 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNINIKGVKPGTTA 236  
Qy 235 SDNVDFVRTYDVEFLSADTKTTVNESKNGKRTVEKIGAKTSVIKEKDGKLVTKGDK 294  
Db 237 SDNVDFVRTYDVEFLSADTKTTVNESKNGKRTVEKIGAKTSVIKEKDGKLVTKGDK 296  
Qy 295 GENGSDTBEGGLVTAKEVIDAVNKGWRMKTITANGQTQADKPFETVSGTNVTFASGK 354  
Db 297 GENGSDTBEGGLVTAKEVIDAVNKGWRMKTITANGQTQADKPFETVSGTNVTFASGK 356  
Qy 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVSPSKG 414  
Db 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVSPSKG 416  
Qy 415 KMDETVINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473  
Db 417 KMDETVINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 476  
Qy 474 KONKPVRTNAPVKEGVDVTNVAQLKGVQNLNNHNDVGNARAGIAQAATATAGLVQA 533  
Db 474 KONKPVRTNAPVKEGVDVTNVAQLKGVQNLNNHNDVGNARAGIAQAATATAGLVQA 533

Db 477 DANKPVRITNAPVKEGVDVTNVAQLKGVQNLNNHNDVGNARAGIAQAATATAGLVQA 536  
Qy 534 YLPGRSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASASVGYQW 591  
Db 537 YLPGRSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASASVGYQW 594

RESULT 9  
US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 91.1%; Score 2736.5; DB 4; Length 594;  
Best Local Similarity 92.0%; Pred. No. 1.6e-204;  
Matches 550; Conservative 11; Mismatches 26; Indels 11; Gaps 4;  
Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASANNEQEDL 60  
Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
Qy 61 YLDPVQRTAVLIVNSDKEGTGEKEKEVEENSDWAYVFNEKGVLTAREITLKAGDNLKIQ 120  
Db 58 YLEPQRTAVLISFSDKEGTGEKEGTEG- SNWAYVFDEKRVLKAGAITLKAGDNLKIQ 116  
Qy 121 -----NGTNFYSLKKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 174  
Db 117 NTNENTNDSSFYSLKKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176  
Qy 175 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNINIKGVKPGTTA 234  
Db 177 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNINIKGVKPGTTA 236  
Qy 235 SDNVDFVRTYDVEFLSADTKTTVNESKNGKRTVEKIGAKTSVIKEKDGKLVTKGDK 294  
Db 237 SDNVDFVRTYDVEFLSADTKTTVNESKNGKRTVEKIGAKTSVIKEKDGKLVTKGDK 296  
Qy 295 GENGSDTBEGGLVTAKEVIDAVNKGWRMKTITANGQTQADKPFETVSGTNVTFASGK 354  
Db 297 GENGSDTBEGGLVTAKEVIDAVNKGWRMKTITANGQTQADKPFETVSGTNVTFASGK 356  
Qy 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVSPSKG 414  
Db 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVSPSKG 416  
Qy 415 KMDETVINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473  
Db 417 KMDETVINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 476  
Qy 474 KONKPVRTNAPVKEGVDVTNVAQLKGVQNLNNHNDVGNARAGIAQAATATAGLVQA 533  
Db 477 DTNKPVRITNAPVKEGVDVTNVAQLKGVQNLNNHNDVGNARAGIAQAATATAGLVQA 536  
Qy 534 YLPGRSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASASVGYQW 591

US-09-669-974-7

	Query Match	90.6%;	Score	2721.5;	DB	4;	Length	598;
	Best Local Similarity	90.9%;	Pred.	No.	2.4e-203;			
	Matches	547;	Conservative	12;	Mismatches	28;	Indels	15; Gaps
Qy	1	MNKYRIIWNLSANLNAWVSELTNHPTKRASATVTAVLATLLFATVQASANNQEEDL	60					
Dbl	1	MNKYRIIWNLSANLVVVSELTNRHTKRASATVATAVLATLLFATVQANATD---	DDDL	57				
Qy	61	YLDPQRFTAVILVNSDKEGTGEKKEVENSOWAYPNEKGVLTAARETLTKAGDNLIKQ	120					
Dbl	58	YLEPQRFTAVVLSFRSDKEGTGEGEKST--SNMAYVFDEKRVLKAGAITLTKAGDNLIKQ	116					
Qy	121	-----NGNTNYSLKKLDLTDLTSVTEKLFSFGANGKNVNITSDTKGLNFAKETAG	170					
Dbl	117	NNTENNTENTNDSSFYSLLKKLDLTDLTSVTEKLFSFGANGKNVNITSDTKGLNFAKETAG	176					
Qy	171	TNGDTVHLINGTGISLTDTLLTCATTNVNTDNVTTDDSKPRASVDVLNAGCNIIKVGP	230					

Qy 590 OW 591



Db 597 QW 598

RESULT 12

```

US-09-669-974-13
: Sequence 13, Application US/09669974
: Patent No. 6333173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 13
: LENGTH: 598
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-13

```

Query Match 90.6%; Score 2721.5; DB 4; Length 598;  
Best Local Similarity 90.9%; Pred. No. 2.4e-203;  
Matches 547; Conservative 12; Mismatches 28; Indels 15;

Qy	1	MNKYRIIWSALNANWAVSELTRHNHTRKRASATVKTAVLATPLLFATVOASANNEEQEBDL	60
Db	1	MNKYRIIWSALNANWVSELTRHNHTRKRASATVATVATLATLLEATVOANATD--DDDL	57
Qy	61	YLDPVQRTAVAVLIYNSDKEGTGEKEKYEENS DWAYVNEKGVLTAREITLLKAGDNLKIKQ	120
Db	58	YLEPVQRTAVAVLSRSDKEGTGEKEGTED-SNNAVYVDEKRVLKAGAITLLKAGDNLKIKQ	116
Qy	121	-----NCTNFTYSLLKDLTDLTSVGTSEKLSFGANGKNVNTSDTKGLNFAKETAG	170
Db	117	NTNENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG	176
Qy	171	TNGDPTVHLNGIGSTLTDTLLENTGATTVNTNDNTVDDEKKRAASVKDVLNAGWNIKGVPK	230
Db	177	TNGDPTVHLNGIGSTLTDTLLENTGATTVNTNDNTVDDEKKRAASVKDVLNAGWNIKGVPK	236
Qy	231	GTTASDNVDVVRTYDTEVEFLSADTKTTTTVNVYESKDNCKTEVKIGAKTSVKEKDGKLVLT	290
Db	237	GTTASDNVDVVRTYDTEVEFLSADTKTTTTVNVYESKDNCKTEVKIGAKTSVKEKDGKLVLT	296
Qy	291	GKDKGNGSSDDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSGTNVTFP	350
Db	297	GKGDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSGTNVTFP	356
Qy	351	ASGKGTTATYSKDDQGNITVMYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVIISGNVYS	410
Db	357	ASGNGTTATYSKDDQGNITVKYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVIISGNVYS	416
Qy	411	PSKGKMDETVNVINAGNNIETIRNGKNIDTATSMTPQFSVSLGAGADAPTLVSVDGD-ALN	469
Db	417	PSKGKMDETVNVINAGNNIETIRNGKNIDTATSMTPQFSVSLGAGADAPTLVSVDDEGALN	476
Qy	470	VGSKKDNKPVRIITNVA PGVKEGDVTNVAQLKGVAQNLNMRIDNDVGNARAGIAQAIATAG	529
Db	477	VGSKDNKPVRIITNVA PGVKEGDVTNVAQLKGVAQNLNMRIDNDVGNARAGIAQAIATAG	536
Qy	530	LVQAYLPCKSMWATGGGTGYRGEAGYAIQYSSISDGGNNIWKGTASGNSRGHFGASAVGY	589

596  
537 LAQALPCKSMIAIGGCTYRGEACYAIGYSSISDTGNWIKGTASGNRCHFGASASVG 596

RESULT 13

```

US-09-377-155-5
: Sequence 5, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK. Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 598
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-5

```

Query Match 90.3%; Score 2712.5; DB 4; Length 598;  
Best Local Similarity 90.5%; Pred. No. 1.2e-202;  
Matches 545; Conservative 13; Mismatches 29; Indels 15;

Qy	1	MNKYIRIWSALNAWVAVSELTRNHHKTRASATVKYTAVALATLLFATVQASANNHEQEEDL	60
Db	1	MNKYSRIWSALNAWVSELTRNHHKTRASATVATAVLATLLFATVQAANATD- --DDDL	57
Qy	61	YLDPVQRTAVLIVNSDKEGTGEKEKVEEYNSDWAIVYNEKGVLTAREITLAKGDNLIKIQ	120
Db	58	YLEPQVQRTAVVLSRSDKEGTGEKEGEDT-SNAWVYFDEKRVLKAGAITLAKGDNLIKIQ	116
Qy	121	-----NGTNFTYSLLAKDLTDLTSVTEKLSFGANGKNKVNITSDTKGLNFAKETAG	170
Db	117	NTNENTNENTNDSFTYSLLKDLTDLTSVTEKLSFGANGKNKVNITSDTKGLNFAKETAG	176
Qy	171	TNGDPTVHLNGIGSTLTDTLTNGTATTNVTNDNVTDDEKKRAASVKDVLNAGNHIKVKXP	230
Db	177	TNGDPTVHLNGIGSTLTDTLTNGTATTNVTNDNVTDDEKKRAASVKDVLNAGNHIKVKXP	236
Qy	231	GTTASDNVDVFRVTDYTFEFLSADTKTTTVNVVESKDNGCKTTEVKIGAKTSVIKEKDGKLYT	290
Db	237	GTTASDNVDVFRVTDYTFEFLSADTKTTTVNVVESKDNGCKRTEVKIGAKTSVIKEKDGKLYT	296
Qy	291	GKDGKNGSSYDDEGEGVLTAKEVIDAYNKAGWRMKTTTANGQTQADKFFETVTSGTNVTF	350
Db	297	GKDGKNGSSYDDEGEGVLTAKEVIDAYNKAGWRMKTTTANGQTQADKFFETVTSGTNVTF	356
Qy	351	ASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGWNLDLSKAVAGSSGKVIISGNVS	410
Db	357	ASGNGTTATVSKDDQGNITVKYDYNVGDALNVQLNSGWNLDLSKAVAGSSGKVIISGNVS	416
Qy	411	PSKGMDETVMINAGNIEITRNCKNIDDIATSWTPQPSVSLGAGADAPTLSDVGDG-ALN	469
Db	417	PSKGMDETVMINAGNIEITRNCKNIDDIATSWTPQPSVSLGAGADAPTLSDVDEGALN	476
Qy	470	VGSKDKNKPVRTINWAPGVKGGDVTNVAQLKGVAOINLNRRINDVGNARAGIAQAATATAG	529
Db	477	VGSKDKNKPVRTINWAPGVKGGDVTNVAQLKGVAOINLNRRINDVGNARAGIAQAATATAG	536
Qy	530	LVQAQYLPCKSMMAIGGGTYRGEAGYAICYGISDSIDGGNWI1KGTASGNSRGHFGASASVG	589

Db 537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVTKGTASNSRGHFGTSASVGY 596  
QY 590 QW 591  
Db 597 QW 598  
RESULT 14  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 90.3%; Score 2712.5; DB 4; Length 598;  
Best Local Similarity 90.5%; Pred. No. 1.2e-202;  
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;  
QY 1 MNKIYRIIWSALNANWAVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEOEEDL 60  
Db 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
QY 61 YLDPVORTVAVLIVNSDKEGTGEKEKEVEENSDWAVYNEKGVLTAREITLAKAGDNLKIQ 120  
Db 58 YLEPVORTVAVLVSRSDKEGTGEKEGTED-SNWAVYDEKRVLKAGAITLAKAGDNLKIQ 116  
QY 121 -----NGTNFTYSLKKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAG 170  
Db 117 NTNNTNNTNDSFTYSLKKDLTDLTSVETEKLSEFANGKNVNTSDTKGLNFAKETAG 176  
QY 171 TNGDTTVHLNGIGSTLTDLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKP 230  
Db 177 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKP 236  
QY 231 GTTASDNVDFVRYDYVEFLSADTKTTTVNYESKDNKKTEVKIGAKTSVKEKDGKLYT 290  
Db 237 GTTASDNVDFVRYDYVEFLSADTKTTTVNYESKDNKKTEVKIGAKTSVKEKDGKLYT 296  
QY 291 GKDKGNGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKPEFTVTSNTVTF 350  
Db 297 GKDKGNGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKPEFTVTSNTVTF 356  
QY 351 ASGKGTATVSKDDQGNITVMYDVNVDALNVNQLNSGNWLDKAVAGSSGKVISGNVS 410  
Db 357 ASGNGTATVSKDDQGNITVMYDVNVDALNVNQLNSGNWLDKAVAGSSGKVISGNVS 416  
QY 411 PSKGMDETWINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALN 469  
Db 417 PSKGMDETWINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALN 476  
QY 470 VGSKDNKPKVRITNVAPGVKEGDTNVAQLKGVAQNINNRIDNVNVDGNRAGTAQAIATAG 529  
|||||

Db 477 VGSKDNKPKVRITNVAPGVKEGDTNVAQLKGVAQNINNRIDNVNVDGNRAGTAQAIATAG 536  
QY 530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVTKGTASNSRGHFGTSASVGY 589  
Db 537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVTKGTASNSRGHFGTSASVGY 596  
QY 590 QW 591  
Db 597 QW 598  
RESULT 15  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 89.5%; Score 2689; DB 4; Length 599;  
Best Local Similarity 89.5%; Pred. No. 8.1e-201;  
Matches 539; Conservative 16; Mismatches 33; Indels 14; Gaps 4;  
QY 1 MNKIYRIIWSALNANWAVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEOEEDL 60  
Db 1 MNKIYRIIWSALNANWAVVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEE- 59  
QY 61 YLDPVORTVAVLIVNSDKEGTGEKEKEVEENSDWAVYNEKGVLTAREITLAKAGDNLKIQ 120  
Db 60 -LEPVRSALVLOFMIDKEGGENEST-GNIGWSIYDHNHTLHGATVTLKAGDNLKIQ 117  
QY 121 -----NGTNFTYSLKKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAG 170  
Db 118 NTNNTNNTNDSFTYSLKKDLTDLTSVETEKLSEFANGKNVNTSDTKGLNFAKETAG 177  
QY 171 TNGDTTVHLNGIGSTLTDLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKP 230  
Db 178 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKP 237  
QY 231 GTTASDNVDFVRYDYVEFLSADTKTTTVNYESKDNKKTEVKIGAKTSVKEKDGKLYT 290  
Db 238 GTTASDNVDFVRYDYVEFLSADTKTTTVNYESKDNKKTEVKIGAKTSVKEKDGKLYT 297  
QY 291 GKDKGNGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKPEFTVTSNTVTF 350  
Db 298 GKDKGNGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKPEFTVTSNTVTF 357  
QY 351 ASGKGTATVSKDDQGNITVMYDVNVDALNVNQLNSGNWLDKAVAGSSGKVISGNVS 410  
Db 358 ASGKGTATVSKDDQGNITVMYDVNVDALNVNQLNSGNWLDKAVAGSSGKVISGNVS 417  
QY 411 PSKGMDETWINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-DALN 469  
Db 418 PSKGMDETWINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALN 477  
QY 470 VGSKDNKPKVRITNVAPGVKEGDTNVAQLKGVAQNINNRIDNVNVDGNRAGTAQAIATAG 529  
|||||

Db	478	VGSKDANKPVRITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIATAG	537
Qy	530	LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRGTASGNSRGRHFGASASVGY	589
Db	538	LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRGTASGNSRGRHFGASASVGY	597
Qy	590	QW	591
Db	598	QW	599

Search completed: September 5, 2002, 10:23:48  
Job time: 285 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 5, 2002, 10:24:32 ; Search time 34.15 Seconds  
(without alignments)  
1662.922 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWNLSALNAWVAYS.....TASGNSRGHFGASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2999	99.9	591	2 G81133	adhesin NMB0992 [i
2	2468.5	82.2	592	2 A81888	probable surface f
3	605	20.1	298	2 I64138	adhesin homolog HI
4	393	13.1	2059	2 D82671	surface protein XF
5	378	12.6	1107	2 AC0976	probable autotrans
6	371.5	12.4	1190	2 A82615	surface protein XF
7	363	12.1	1588	2 A86036	probable adhesin Z
8	363	12.1	1588	2 H91188	probable adhesin E
9	331.5	11.0	658	2 AH0110	probable surface p
10	240.5	8.0	1004	2 C82672	surface-exposed ou
11	235.5	7.8	1091	2 G64964	hypothetical prote
12	232.5	7.7	1536	2 A43855	high-molecular-wei
13	221	7.4	1477	2 B43855	high-molecular-wei
14	221	7.4	2020	2 C48399	ABC-type transport
15	219	7.3	1910	2 AF0394	probable adhesin h
16	214	7.1	4919	2 T31105	hypothetical prote
17	213.5	7.1	5291	2 F90696	hypothetical prote
18	212.5	7.1	1286	2 S28634	adhesin AIDA-I pre
19	212	7.1	949	2 D90803	AIDA-I adhesin-lik
20	212	7.1	1005	2 H85611	probable adhesin Z
21	212	7.1	1635	2 A10452	hemolysin [importe
22	211	7.0	1109	2 A56143	surface-array prot
23	210	7.0	1325	2 A64905	ydeK protein - Esc
24	209	7.0	2273	2 T09083	hemagglutinin/hemo
25	208.5	6.9	936	2 I40711	sapB protein - Cam
26	208.5	6.9	1018	2 H83135	probable adhesin P
27	207.5	6.9	1577	2 A35140	hemolysin A precur
28	207.5	6.9	4152	2 T31102	filamentous hemagg
29	207	6.9	5188	2 B85547	probable RTX famil

ALIGNMENTS

RESULT 1

G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.K.; Haft, D.H.; Salzberg, S.B.; White, O.; Fleischmann, R.D.; Dougherty, B.; Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TET>  
A:Cross-references: GB:AF002450; GB:AF002098; NID:g7226229; PIDN:AAF41395.1; PID:g7222  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match	Best Local Similarity	Score	DB 2:	Length	591;
Matches	590; Conservative	99.8%;	0; Mismatches	1; Indels	0; Gaps
Qy 1	MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDL	60			
Db 1	MNKIYRIIWNLSALNAWVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDL	60			
Qy 61	YLDPVQRTVAVLIIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLIKQ	120			
Db 61	YLDPVQRTVAVLIIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLIKQ	120			
Qy 121	NGTNTFTYSLKKDLTDLTTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGTNGDVTTHLN	180			
Db 121	NGTNTFTYSLKKDLTDLTTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGTNGDVTTHLN	180			
Qy 181	GIGSTLDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDF	240			
Db 181	GIGSTLDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDF	240			
Qy 241	VRTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKDGENSS	300			
Db 241	VRTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKDGENSS	300			
Qy 301	TDEGSLVTAKEVIDAVNKAGWRMKTTTANGOTGADKFEETVTSCTNNVTFASSKGTATV	360			
Db 301	TDEGSLVTAKEVIDAVNKAGWRMKTTTANGOTGADKFEETVTSCTNNVTFASSKGTATV	360			
Qy 361	SKDDQGNITVMYDVNVGOALNVNLQNSGNWLDLSKAVAGSSGKVISGNVSPSKGMDETV	420			

Db 361 SKDDGNTWYDYNVGDALNVQNLONGWNLDSKAVAGSGKVISGNVSPSKGKWDIV 420  
QY 421 NINAGNNIETRNGKNIDTATSWTFOFSSVSLGAGADAPTLSDVDGALNVGSKDNKPVR 480  
Db 421 NINAGNNIETRNGKNIDTATSWTFOFSSVSLGAGADAPTLSDVDGALNVGSKDNKPVR 480  
QY 481 ITNVAPGVKGDVTNVQAUKGVAQNLNNRDNVDGNRAGTAQIAIATAGLVQAYLPGKSM 540  
Db 481 ITNVAPGVKGDVTNVQAUKGVAQNLNNRDNVDGNRAGTAQIAIATAGLVQAYLPGKSM 540  
QY 541 MAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 2  
A:1888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Paikhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
K.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moutre, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match 82.2%; Score 2468.5; DB 2; Length 592;  
Best Local Similarity 84.4%; Pred. No. 1.7e-114;  
Matches 507; Conservative 30; Mismatches 45; Indels 19; Gaps 8;

QY 1 MNKIYRIIWSALNANNAVAVSELTRNHTKRASATVKTVATLTLFAVQASANNEQEDL 60  
Db 1 MNKIYRIIWSALNANNAVAVSELTRNHTKRASATVKTVATLTLFAVQANATDEDEEB- 59  
QY 61 YLDPVQRTAVLVNSDKEGTGEKEKVE-ENSDWAVYFNEKGVLTAREITLKAGDNLIK 119  
Db 60 -LESVQSRV-VGSIQASMEGSGELETSLSWTDNSKEFVDPYIV---VTLKAGDNLIK 113  
QY 120 Q-----NGNTFTYSLKDLTDLTSVGTGKLSFSGANGKNVNTSDTKGLNFAKETAGT 173  
Db 114 QNTNENTNASFTYSLKDLTGLINVTETKLSFGANGKNVNTSDTKGLNFAKETAGT 173  
QY 174 DTTVHLNIGSTLDTLLNTGATNTVNDVDEKKRAASVKDVLNAGNNIKGVKPGTT 233  
Db 174 DTTVHLNIGSTLDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGNNIKGVKGTST 231  
QY 234 A--SDNVDFVRTYDTVEFLSADTKTTTVNVEKDKGKKEVTKIGAKTSVIKEKDKGLVTG 291  
Db 232 TGQSENDFVRTYDTVEFLSADTKTTTVNVEKDKGKKEVTKIGAKTSVIKEKDKGLVTG 291  
QY 292 KDKGENSGTDEGEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEVTSNTVTF 351  
Db 292 KDKGENSGTDEGEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEVTSNTVTF 351  
QY 352 SKGKTATVSKDDOGNITWYDYNVGDALNVQNLONGWNLDSKAVAGSGKVISGNVSP 411  
Db 352 SKGKTATVSKDDOGNITWYDYNVGDALNVQNLONGWNLDSKAVAGSGKVISGNVSP 411  
QY 412 SKGKMDETVINAGNNIETRNGKNIDTATSWTFOFSSVSLGAGADAPTLSDVDG-ALNV 470  
Db 412 SKGKMDETVINAGNNIETRNGKNIDTATSWTFOFSSVSLGAGADAPTLSDVDGALNV 471

QY 471 GSKKDNKFPVRIITNVAPGVKEGDVTNVQAUKGVAQNLNNRDNVDGNRAGIAQAATATAGL 530  
Db 472 GSKDANKPVRITNVAPGVKEGDVTNVQAUKGVAQNLNNRDNVDGNRAGIAQAATATAGL 531  
QY 531 VQAYLPKSKMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 590  
Db 532 VQAYLPKSKMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 591  
QY 591 W 591  
Db 592 W 592

RESULT 3  
I64138  
adhesin homolog H1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: I64138  
R:Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.1%; Score 605; DB 2; Length 298;  
Best Local Similarity 45.9%; Pred. No. 4.4e-23;  
Matches 145; Conservative 42; Mismatches 93; Indels 36; Gaps 8;

QY 1 MNKIYRIIWSALNANNAVAVSELTRNHTKRASATVKTVATLTLFAVQASANNEQEDL 60  
Db 1 MNKIYRIIWSALNANNAVAVSELTRNHTKRASATVKTVATLTLFAVQASATVQA----- 49  
QY 61 YLDPVQRTAVLVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLIK- 119  
Db 50 -INDAGTFVKVQSTEDIEDSAATK--DDKNQALKAGD-----TLTKAGKNNLAKL 99  
QY 120 -QNGTFTYSLKDLTDLTSVGTGKLSFSAN-----GNKVITSDTKGLNFAKETAGT 171  
Db 100 DQGGKSVTFALAKDLVDVTKAVSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK---GT 156  
QY 172 NGDTTVHLNIGSTLDTLLNTGATNTVNDVDEKKRAASVKDVLNAGNNIKGVKPG 231  
Db 157 NGDTAVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKTRAATIKDVLNAGNNIKGAKVA 215  
QY 232 TTASDNVDVVRTYDTVEFLSADTKTTTVNVEKDKGKKEVTKIGAKTSVIKEKDKGLVTG 291  
Db 216 GGNTENVDLVAGVDNVFEITGDKNLDVLVTAKEGKTTTEVKPTKTSVIKONNGKLLTG 275  
QY 292 KD--KGENGSTDEGE 305  
Db 276 KQLKDANTGATNATE 291

RESULT 4  
D82671  
surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below



Db 862 ENGIGDIVTGTGTYFKTNTDGDADANAQAGDSVAIGSGSIAAAENSVALGTNSVADEANT 921  
Qy 468 LNVGSKDNKPKVRIITNAPGVKEGDTNVAQLK----- 500  
Db 922 VSVGSSTQQR--RIITNVAAGVNTDVAQVQLKASEAGSVRYETNADGSVNYSVLNLGDG 979  
Qy 501 -----GVAAO----- 523  
Db 980 SGGTRIGNVSAVNDTDAVNYAQLKRSVEANYYTDQKMGEMNSKIKGINKMGGGAS 1039  
Qy 524 AIATAGLVQVLYPKSMMAIGGTYRGAGYAIGYSSISDGGNWIITKGTASNSRHFGEA 583  
Db 1040 AMAGLUPQAYAPGANNMTSIAGGTNGESAVAIAGVMSVSGGWYTKLQGTNSOGDYSA 1099  
Qy 584 SASVGYQW 591  
Db 1100 AIGAGFOW 1107  
  
RESULT 6  
A82615  
surface protein xfi981 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82615; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1190 <STM>  
A:Cross-references: GB:AE004017; GB:AE003849; NID:99107083; PIDN:AAF84783.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, P  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: Xfi981  
  
Query Match 12.4%; Score 371.5; DB 2; Length 1190;  
Best Local Similarity 23.5%; Pred. No. 8.le-11;  
Matches 167; Conservative 88; Mismatches 243; Indels 213; Gaps 28;  
  
Qy 17 VAVSELTRNHTKRASATVKTAVLATLIPATVQASANNEDDELYLDPVQRT-----VAV 71  
Db 557 VTSGISAGNQKITNVAAGTADTDAVNFSQLQAVSVSTASKGNWLLASGANSNSVVPGESV 616  
Qy 72 LLYNSDKETGEKEKVEENSOWAYFNEKGVLTAREIT-----LKAGDNLKIKQN 121  
Db 617 DLKNSD--GNLLTKTTDSND--VTFNLATALKVDSLTTGTANTMTDGTGVTGNSVNTLGS 672  
Qy 122 GTNFTYSLKKDLTDLTSVGTETKLSFANGKNV-NI---TSDTKGLNFA----- 165  
Db 673 GLVIT-----DGPSTSSG-----ISAGNQKITNVAAGTADTDAVNFSQLQAVSVSTASKG 722  
Qy 166 -----KETAG----- 178  
Db 723 WLLASGANSNSVAPGESVDLKNKTGDNIVISKESGSDVLFNLSSSLKDLKLTGDTWT 782

## RESULT 7

A86036  
Probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A86036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamasis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:912518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029

Query Match 12.1%; Score 363; DB 2; Length 1588;  
Best Local Similarity 24.7%; Pred. No. 3.le-10;  
Matches 145; Conservative 78; Mismatches 228; Indels 136; Gaps 22;  
  
Qy 121 NGNFTYSLKKDLTDLTSVGTETKLSFANGKNV-ITSDDTKGLNFAKETAGTNGDTTVHL 179  
Db 1022 NATNMIEQNTQIINOLAGNTDATYIQENGAGINVTNDGDLAFNDASAQGVGATAIGY 1081  
Qy 180 NGI-----GSTLTDTLNTGA-TTNVTNDNV-----TDDE 208  
Db 1082 NSVAKGSSVAIQGGSYSDVTGIALGSSSVSRVIAKSRDTSITENGWVIGYDTTDE 1141  
Qy 209 KKAASVKD-----VLNAGWNKIKGPGTTASDNVDFVRYDTVEFLSADTKTTVNVE 262  
Db 1142 LLGALSIGDDGKYRIIN-----VADGSEHDAVT-VROLQNAICAVATPTTKYFAN 1193  
Qy 263 SKDNGK-----KTEVKIGAKTSVIREK-----DGKLVTKCKDGE----- 296



Db	1194	STEDSLAVGTTDSLAKAKTIIVNGDKGIGIGYGVADVADANALNGIAISNAQVHIVNSIAI	1253
Qy	297	-NGSSTDGEGLVTAKEVIDAVNKAQWRMKTTTANGQ-----TGQADKPETVTSCTNV	348
Db	1254	NGSSTTRGAQTNVYATYNMDAQNSVGEESVGSADGQRLITNVAAGSAD-----TDVNV	1308
Qy	349	TFASGKGTATVSKDDQGNITVW-----YDVNVGDAL-----NVNQL	385
Db	1309	--GOLKVTDQAQVSQNTQ-SITNLDNRVTNLDNRVTNIENGIGDIVTGTSTKYFKYKNTDGV	1365
Qy	386	QNSGWNLDKAVAGSCKVIGSNVSPSKGM---DETVINAGNNIETRN---GKN---	436
Db	1366	DASAQKQDSVAIGSGSIAAADNSVALGTGSVATEENTISVGSSTNORRITNVAAGKNATD	1425
Qy	437	-IDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDNKPNRITNVAPVKGQDVTN	495
Db	1426	AVNVQALKSEAGGVRYDTRKDG---SIDYSNITLGG-GNGGTTTRISNVSGVNNNDVVN	1481
Qy	496	VAQLKGVAQ-----NLNNRIDNVGNARAGIAQAATAGLVOAYLPGKSMMAIG	544
Db	1482	YAQLKQSVQETKQYTDQRMVEMDNKLSKTESKSGSIASAMAMTGLPAYTPGASMASIG	1541
Qy	545	GGTYRGAGVAICYSSISDGGNWIKTGTASNGSRGHFGASASGVQW	591
Db	1542	GGTYNGESAVALGVMSVANGRWYVKLOGSTNSOGEYSAAALCAGTOW	1588

RESULT 8  
H91188  
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_rev18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <MAX>  
A:Cross-references: GB:BA000007; PIDN:BA37903.1; PID:gl13363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECS4480

Query Match	12.1%	Score 363;	DB 2;	Length 1588;			
Best Local Similarity	24.7%;	Pred. No. 3.1e-10;					
Matches	145;	Conservative	78;	Mismatches 228;			
			Indels	136;			
			Gaps	22;			
Qy	121	NGTFTYSLKDLTDLTSVGTKEKLSFSANGKNVN-ITS	DTKGLNFAKETA	CTAGTGGTTVHL 179			
			:	:			
Db	1022	NATNMITEQNTQIIINQLAGNTDATYIQENGAGIN	YVVRTDDGLAFND	ASAOQGVATAICY 1081			
		:	:	:			
Qy	180	NGI-----	-----G	STLTDLLNTGA-TTNVTNDNV-----TDDE 208			
			:	:			
Db	1082	NSVAKGSSVAIGQGSYSDVDTGTALGSSSVSSRV	AKGRSDTSITENG	VIGYDTTDGE 1141			
		:	:	:			
Qy	209	KKRAASVKD-----	VLNAGNINIKVG	PGGTTASDNVDFVRYDTVEE	LSADTKTTTNNVE 262		
			:	:			
Db	1142	LLGALSIGDCKYRQIIN-----	VADGSEAHDAVT-V	RQLQNAIGA	VAVATTPKYFPHAN 1193		
		:	:	:			
Qy	263	SKDNKG-----	KTEVKIGAKTSV	IREK-----	DGKLVTGDKDGE----- 296		
		:	:	:			
Db	1194	STEEDSLAVGDSL	AMGAKTIVNGDK	GIGYGAVVDANAL	NGIAIGSNAQVIHVN	STAI 1253	
		:	:	:			
Qy	297	-NGSSTDBEGLV	TAKEVIDAVN	KAGWRKMTTANGQ-----	TGQADKFTETV	SGTNNV 348	
			:	:			
Db	1254	GNGSTTTTRGAT	NTNTAYNMAD	PQNSVGEFSVGS	ADGQRQITNV	AAGSAD-----TD	VANN 1308
		:	:	:			
Qy	349	TFASGKGTTATV	SKDDOGNIATM-----	YDVNVGDAL-----	NVNOL 385		

Db 1309 --GOLKYTDQAVSQNTQ--SITNLNDRVTNLDSRVNTIENGIGDIVTTTGSTKYFKTNDGV 1365  
QY 386 QNSCWNLDSKAVAGSSGKVIISGNSPSKGM---DETVINAGNNIEITRN---GKN--- 436  
Db 1366 DASAQGKDSVAIGSGSTAADNSVALGTGVSATENTISVGSSTNQRRITNVAAGKATD 1425  
QY 437 -IDIATSMTPQFSSVSLGACADAPTLSDGDLNVGSKKDNKPVRIITNVAPGVKEGDVTN 495  
Db 1426 AVNVAQLKSSSEAGGVRYDTRADG---SIDYSNITLGG--GNGGTTTRISNVSAGVNNNDVN 1481  
QY 496 VAQLKGVQAQ-----NLNRRIDVDCNARAGTAQAATATAGLVAQVLPCKSMMAIG 544  
Db 1482 YAQLKQSVQETKQYTDQRMVEMDNKLSKETLSGGISASAMWTGLPQATPGASMASIG 1541  
QY 545 GTTYRGAGVAIGYSSTSDGGNWIIKKTASGNSRGHFGASASVGYQW 591  
Db 1542 GGTNGESAVALGVSMVSANGRWYKLGQSTNSQGEYSALGACIQW 1588

RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.M.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:gl5978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match	11.08;	Score	331.5;	DB	2;	Length	658;
Best Local Similarity	25.2%;	Pred. No.	3.6e-09;				
Matches	132;	Conservative	74;	Mismatches	204;	Indels	113;
Gaps	22;						
Qy	101	GVLFAREITLKAGDNLIKQNGTFTYSKXKDLDTLTSVGTSEKLSFSANGKXNVITSDTK	160				
Db	217	GAVTISQANSIALG--AASINTVGAOSSYSAYALTAPOASVSGELGIC-FALGNR-KITGVAA	273				
Qy	161	GLNFAKETAGTNGDPTVHLNNGIGSTLTDLTLLTGATTNVTN--DNVTDDEKKRAASKVD	218				
Db	274	G-----SASSDAVNVAQLTAVGQVQOQ-----TANITSLGRVVTIE-----GSMASI	317				
Qy	219	LNAGWNITKGVPKGTASDNVDVFRTYDVFELSDATKTTTNNVSKONGKKT-----EV	272				
Db	318	ANGG-GVKYFIHANTQPDV-----ASGTNSVAIGPASLASGNNAALASGAGAV	364				
Qy	273	KIGAKTSVIKBDKGLVTGDKDGENSGSTDEGELVTAKEVIDAVNKAGWRMKTTTANGQ	332				
Db	365	AIG--DGAASASDGSVAIGQSGDNGRGVENVIG-----KYSNASNTS	405				
Qy	333	TGQADKKEFTVTSNTNVTFAASKGCTTATVSKDDQGNITVMYDVNVGDALNVQLNSGNHL	392				
Db	406	SG-----TVSVGNTAT-----GETRTVSNVADG-----LQATDAVNLROLDG-----	442				
Qy	393	DSKAVAGSSGRKVISGNVSPSKMKDEVTNINAGNNI--EITRNGKNIDI--ATSMTPQPFSS	449				
Db	443	-----IAASIVVENVNYSGLQNTDGMFQVNNSSGLAKPSATGANSATCGAGSVASGNNNS	497				
Qy	450	VSLGAGADAP-----TLSDVDGALNVGSKKDNKPKVRITNVAPGVKEGDVTNVAQL	499				
Db	498	TAFSGSGAKATAANGAALGANSVADRANSVSGVGNR--QITNVAPATQCTDAVNFQDL	555				



Qy 275 G-AKTSVKEKDGKLVTKGKNGSGSTDE---GEGLV-----TAKEVIDAVNKAQRW- 324  
Db 280 GTANTTV-----YAGGDQTVHGHALDTTLNGGYQYVHNGGTASDTV--VNSDGMQIV 330  
Qy 325 -----KTTTANGOTGQADKFEVTSGTNVTFASG---KGTATVSKDDOG-NITVMYD 373  
Db 331 KNGVAGNTTVN-QKGRU-QVDAGGTATNVTLKOGGALVTTAAATVT-----GINRLGAFS 384  
Qy 374 VNVGDALNVQLNSGWNLDKAVAGSSGKVISGNSVSPSKMDETVINAGNIEIRN 433  
Db 385 VVEGKADNV-VLENGG-RLD-----VLTGHTATN-----TRVDDGGTLDV-RN 424  
Qy 434 GKNIDTATSMTPQPFSSVSLGAGADAPTLSDGDALNVGSKDKNDKPKVRTITNVAPGKEDV 493  
Db 425 G-----GTATT-----VSMNGG---VLLADSGAAVSGTRSDGK-----AFSIGGQOA 464  
Qy 494 TNVAQLKGVAQNLRNIDNVGNARAGTAQAATATAGLVQAYLPCKSMMAIGGTYRGEAG 553  
Db 465 DALMLERGSSTLN-----AGDTATDTT-----VNGGLUFTARGG 498  
Qy 554 YAIGYSSISDGGNWIIRKGTASGN 576  
Db 499 TLACGTTLNNGAILTSLCKTVNN 521

RESULT 12  
A43855  
high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae  
C:Species: Haemophilus influenzae  
C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: A43855  
R:Barenkamp, S.J.; Leininger, E.  
Infect. Immun. 60, 1302-1313, 1992  
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus pertussis.  
A:Reference number: A43855; MUID:92192797  
A:Accession: A43855  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1536 <BAR>  
A:Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIIP:89239)

Query Match 7.7%; Score 232.5; DB 2; Length 1536;  
Best Local Similarity 22.38; Pred. No. 0.00079;  
Matches 133; Conservative 86; Mismatches 228; Indels 149; Gaps 26;

Qy 40 ATLLFATVOASANNEQEEDLYLDPVQRTVAVLIYNSDKEGTGEKEVEENSDWAVYFNE 99  
Db 778 SSLRFKTSSTKTFPSIEKDLTLNATGGNITLLQV-----EGTDGMI---G 820

Qy 100 KGVLTAREITLKAGNLKIKONGNTFTYSLKDLDTLSVGTKEKLSFSAANGKVNITSD- 158  
Db 821 KGIIVAKKNITFEGG-----NITFGSKAVTEIEG-----NVTINNANVTILIGSDF 866

Qy 159 --TKGLNFAKE-----TAGTN-----GDTTVHLNGIGSTLDTLLNTCAT--TNVTN 201  
Db 867 DNHQRLPIKKDVIINSNLNLAGGIVNAGNLTVESNANFKAITNFTFNVGGLFDNKN 926

Qy 202 DNVTDDEKRAASVDVLNAGNVIKVPAGTASDNVDVFRYDTVEFLSADTKTKTTVNV 261  
Db 927 SNIS--IAKGGARFKDIDS---KNLSITTNSSS-----TYRTIISGNITNKGDLNI 974

Qy 262 ESKONGKKEVIGAKTSVIEKDGKLVTKGDK-----GENSGSDEDEGLVTA 310  
Db 975 TNE--GSDTEMQIGDVS---QKEGNLTISSDKINITKQITIKAGVDGENSDS----- 1022

Qy 311 KEVIDAVNKAQRWKTITANGOTGQADKFEVTSGTNVTFASGKGTATATVSKDDOQNTIV 370  
Db 1023 ----DATNANLTIKT-----KELKLTQDLNI---SGFNKAEITAKD--GSDLT 1062

Qy 371 MYDVNVGDALNV-----NQLNSGWNLDKAVAGSSGKVISGNSVSPSKMDETVINAG 425  
Db 1063 IGTNSADCTNAKKVTFNQVKDSKISADGHKVTLHSHKSVETSGSNNNTDSSD----- 1114

Qy 426 NNIETRNCKNIDTATSMTPQPFSSVSLGAGADAPTLSDGDALNVGSKDKNDKPKVRITNVA 485  
Db 1115 NNAGLTIDAKKNVTNNIT-SHKAVSISATSGEITTKT-GTTINATTGNVEITAGTGSIL 1172

Qy 486 PGVK--EGDVTNVVAOLKGVAQNLRNIDNVGNARAGTAQAATATAGLVQAYLPCKSMMAI 543  
Db 1173 GGIESSSGSVTLTATEGALA-----VSNISGNTVTVTANSALTTLAGSTIKGTESVYT 1226

Qy 544 G-----GGTYRGEAGYAIGYSSISDGGNWIIRK-----GRASGNS 577  
Db 1227 SSQSGDIGGTISGGTVEVKATESLTTQSNKIKATTEANVTSAATGTTGGTISGNT 1282

RESULT 13  
B43855  
high-molecular-weight surface-exposed protein - Haemophilus influenzae  
C:Species: Haemophilus influenzae  
C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
C:Accession: B43855  
R:Barenkamp, S.J.; Leininger, E.  
Infect. Immun. 60, 1302-1313, 1992  
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus pertussis.  
A:Reference number: A43855; MUID:92192797  
A:Accession: B43855  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1477 <BAR>  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:89237, NCBIIP:89240)

Query Match 7.4%; Score 221; DB 2; Length 1477;  
Best Local Similarity 22.6%; Pred. No. 0.0028;  
Matches 139; Conservative 92; Mismatches 231; Indels 152; Gaps 30;

Qy 11 SALNVAWVASELNRHT---KRASATVKTAVLATLLFATVQASANNEQEEDLYLDPVQR 67  
Db 821 NAINSTYINISILGGNVTLLGGQNSSSI-TGNITIEKAANVTLEANNAPNQONI-RDRVIK 878

Qy 68 TVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITL---KAGDNLKIKONGTN 124  
Db 879 -LGSLLVNGSLNGENADI-----KGNLTISESATFKGKTRDTLNTGNFTN 925

Qy 125 FTYSLKDLTDLTSVGTKEKLSFSAANGKVNITSDTK-----GLNFAKET 168  
Db 936 -NGTAEINITQ---GVVKLGNVTDGDLNITTHAKRNQORSIIGGDIINKKGSINI--- 976

Qy 169 AGTNGDTTVHLNGIGSTLDTLLNTGATNVT-----NONVTDE 208  
Db 977 TDSNNDAIEIQGNISQKEGNLTISSDKNITKQITIKKIDGEDSSSDATSNALTI- 1035

Qy 209 KKRAASVDVLNAGNVIKVPAGTASDNVDVFRYDTVEFLSADTKTKTTVNVESKDKGK 268  
Db 1036 TKELKLTDELISISGEN---KAEITAKDGRDLTICNSNDGNSGCAKVTTFN-----NVK 1086

Qy 269 KTEVKIGAKTSVIREKDGKLVTKGDKGSGSSTDEGEGL-VTAKEVIDAVNKAQRWKTIT 327  
Db 1087 DSKISADGHNVTL---NSKVKTSSSNGGSGRESNDNDTGLTITAKNV--EVNKDITSLKTV 1141

Qy 328 TANGOTGQADKFEVTSGTNVTFASGKGTATATVSKDDOQNTIVTVDVNVGDALNVQLN 387  
Db 1142 NIT-----ASEKVTTTAGSTINATNGKASITTKTGDISGTIS-----GNTVSVSA--- 1186

Qy 388 SGWNLDKAVAGSSGKVISG--NVSPSKMDETVINAGNIEIRNCKNIDTATSMTP 445  
Db 1187 ---TVDLTKSGSKIEAKSGEANVTSAATGTTGTTI---SGNTVNVNATAGDITVG----- 1235

Qy 446 QFSSVSLGAGADAPTLSDGDAL--NVGSKDKNDKPKVRITNVAPGVEGDVTNVAQLKGVA 503

Db 1236 --NGAETATEGAATITATGNTLATEAGSS-----ITST-----KGVDLLAONGSIA 1281  
Qy 504 QNLNRRIDNVGNARAGIAAATAGLVQAVLPKSMMAIGGTYRGEAGYAIGYSSISD 563  
Db 1282 GSIN--AANVTLN-----TTG-----TLTTVAGSDIKATSG-----TLVIN 1315  
Qy 564 GGNIIKRTASGNS 577  
Db 1316 AKDALKNGDASGDS 1329  
RESULT 14  
C48399  
ABC-type transport protein ydbA.2 - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 19-Nov-1993 #sequence\_revision 16-Oct-1998 #text\_change 08-Oct-1999  
C:Accession: C48399; D64891; H64891  
R:Mooser, I.; Glaser, P.; Danchin, A.  
Biochimie 73, 1361-1374, 1991  
A:Title: Multiple IS insertion sequences near the replication terminus in Escherichia coli  
A:Reference number: A48399; MUID:92190338  
A:Accession: C48399  
A:Molecule type: DNA  
A:Residues: 464-2020 <MOS>  
A:Cross-references: GB:D85081; NID:93041754  
A:Experimental source: strain K-12  
A:Note: Sequence inconsistent with the nucleotide translation  
A:Note: Sequence extracted from NCBI backbone (NCBIN:88089, NCBI:P:88090)  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: D64891  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-839, 'LDLPLFQRTSVT' <BLA1>  
A:Cross-references: GB:AE000237; GB:U00096; NID:gl787665; PIDN:AAC74483.1; PID:gl787668;  
A:Experimental source: strain K-12, substrain MG1655  
A:Accession: H64891  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-915, 915-2020 <BLA2>  
A:Cross-references: GB:AE000237; GB:U00096; NID:gl787665; PIDN:AAC74487.1; PID:gl787672;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics: GTG  
A:Gene: ydbA.2  
A:Start codon: GTG

Query Match 7.48; Score 221; DB 2; Length 2020;  
Best Local Similarity 23.68; Pred No. 0.0041;  
Matches 167; Conservative 75; Mismatches 230; Indels 236; Gaps 40;  
Qy 50 SANNREEDLYDPVQRTV---AVLVNSDKEGT-----GEKEV-----EENS 92  
Db 141 SPNN-----DVLDTKTLTROSVFYTYENADGTLSDSGRKRATINLWQIDEANNT 195  
Qy 93 WAV-----YENEGVLTAREITLKGDNLIKONGTFTYSLKKDLTDLTSVGT 141  
Db 196 VALEGVSADGATKQWYNHNGELVI-----TGDATVNNNG-----KTIVDGDSTGT 242  
Qy 142 E-----KLSPSANGKNYNTSDT-----KG-----LNF 164  
Db 243 EINGNNGKVIQDGLDVSGGCHGIDITGDSATVDNKGTTVTPESMGIQDGDKAIVNN 302  
Qy 165 AKETAGTNGDTTVHLNG-----IGSLTDLTLNLTGATTVNTDNVTDDEKRAASVKD 217  
Db 303 EGESTITNGTGTQINGDDATANNNGKTTVDGKDSGTGEINGNKGKVIQD-----GDLD 356  
Qy 218 VLNAGWNKGVPGGTASDNVDFVRYDTVEF--LSADTKTTTVNVESKD----- 265

Db 357 VSGGGHGI-DITGDSATVDNKGKTMVTPDESIGIQVDGDQAVVNEGESAITNGGTGTQI 415  
Qy 266 NGKTEVKIGAKTSVKEKDKGLVTGKD-KGEG-----SSTD 302  
Db 416 NGDDATANNNGKTV---DGKDSGTGTETIAGNKGKVIQDGLDVSGGGHIGDITGDSATV 471  
Qy 303 EGEGLVTAKE-----VIDA-----VNKAGWRMKTITANGOTGQADRFETVTSNTVTFAS 352  
Db 472 DNKGTMTVTPDESIGIQDGDQAVVNEG-----ESTITNGGTG-----TQINGNDAT-AN 521  
Qy 353 GKGTATVSKDD-----QGNITVMYDVNGDALNV-----NOLQNSGN--LDSK-----A 396  
Db 522 NSGKTTVDGKDSGTGTKIAGNIGI---VNLDGSLVTGGAHGVENIGDNGTVNKGDIVVS 578  
Qy 397 VAGSSGKVISGNVSPSKGMDTETVINAGNIEITRGNKIDTIATSM-TPQFS----- 448  
Db 579 DTSGIVLNGEGATVSTNGDVNVS-NEATGFSITTTNSGKVSLAGSMQVGDSTGVDLNG 637  
Qy 449 ---SVSLGA-----GADAPTLSDGDALNV---GSKDKNKPVRITNVA-----PGV--- 488  
Db 638 NNSSVTLAARDKLVVQKATGINVSGDANTVITGNVLVDKDKTADNAAEYFFDFSVGIN 697  
Qy 489 ---KEGDTNVNAOLKQVQON-LNNRIDNV-DGNARAGIAQAIATAGLV----- 531  
Db 698 VYGSDDNNVTLDGKLVVSDSEVTSRQSNLFDGSAE-----KTSGLVVGDTNVMNG 750  
Qy 532 -QAYLPKSKMMAIGGTYRGEAGYAI-----GYSSISDGGNIIKG 571  
Db 751 GLELIGEKNALADGSGQVTSRLRTGYSTYSVIVVSGSSVYLNGLDITISG 798  
RESULT 15  
AF0394  
Probable adhesin hmwA [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AF0394  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.  
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0394  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-1910 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:gl5981183; GSPDB:GN00175  
C:Genetics:   
A:Gene: hmwA

Query Match 7.38; Score 219; DB 2; Length 1910;  
Best Local Similarity 20.58; Pred No. 0.0048;  
Matches 148; Conservative 92; Mismatches 255; Indels 228; Gaps 28;  
Qy 14 NAMVAVSEITRNTKRASATVKTAVLATLIPATVQ-----ASA 51  
Db 898 NATITANNISMN---GNITANDAVLMTNITFLAKGDIKDLTSPKGLWFRGNGMTAA 953  
Qy 52 NNEEQEEDLYDPVQRTVAVLVNSDKEGTGEKEVENSADWAVYENKGLTAREITLK 111  
Db 954 NN-----ILLVANS--TSSGETVKINASS-----NKNMNTAGKDISII 990  
Qy 112 AG-----DNLKIKONGTFTYSLKKDLTDLTSVGTETKLSFSAANGKNYNTSDT 159  
Db 991 AGNSKATGPNINIENVALETNNGFT-----TNGITSTLWLCVNVNSANG--VDITSNS 1042  
Qy 160 KGLNFAKETAGTNGDTTVHLNGIGSLTDLTLNLTGATTVNTDNVTDDEKRAASVKD- 218  
Db 1043 TG-----TGGIVLDTNLTITVGD-----INT-IVTNSGKGIIWKSNTSLNSKDI 1089  
Qy 219 ---LNAGWNKGV--KPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKGKTEVK 273



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:31:01 ; Search time 19.11 Seconds  
(without alignments)  
1197.449 Million cell updates/sec

Title: us-09-700-293-4

Perfect score: 3003

Sequence: 1 MNKIIRIWNLSALNRAWVS.....TASGNSRGHFGASASVGQW 591

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	235.5	7.8	1039	1 AG43_ECOLI	P39180 escherichia
2	221	7.4	2003	1 YDBA_ECOLI	P33666 escherichia
3	212.5	7.1	1286	1 AIDA_ECOLI	Q03135 escherichia
4	210	7.0	1325	1 YDEK_ECOLI	P32051 escherichia
5	207.5	6.9	1577	1 HLYA_PROMI	P16466 proteus mir
6	201	6.7	1654	1 OMPB_RICRI	Q53047 r outer mem
7	191.5	6.4	1608	1 HLYA_SERMA	P15320 serratia ma
8	191	6.4	2249	1 OMPA_RICRI	P15921 rickettsia
9	189.5	6.3	1953	1 BIGA_SALTY	P25927 salmonella
10	186.5	6.2	1655	1 OMPB_RICCN	Q9Kka3 r outer mem
11	185	6.2	1645	1 OMPB_RICTY	P96989 r outer mem
12	183	6.1	1007	1 Y741_CHLMU	Q9pj16 chlamydia m
13	182	6.1	917	1 HXA3_HAEIN	P45355 haemophilus
14	181	6.0	1656	1 OMPB_RICJA	Q06653 r outer mem
15	180.5	6.0	928	1 HXA2_HAEIN	P45354 haemophilus
16	180.5	6.0	933	1 SLAP_CAMFE	P35827 campylobact
17	180.5	6.0	1569	1 YPJA_ECOLI	P52143 escherichia
18	180	6.0	2334	1 WAPA_BAGSU	Q07833 bacillus su
19	176	5.9	1861	1 APU_THETU	P38536 t amylopull
20	175.5	5.8	1567	1 ICEN_XANCT	P18127 xanthomonas
21	175	5.8	2021	1 OMPA_RICCN	Q52657 rickettsia
22	174	5.8	918	1 YWJB_CAEEL	P34487 caenorhabdi
23	167.5	5.6	1148	1 ICEP_PSESX	Q30611 pseudomonas
24	167	5.6	1643	1 OMPB_RICPR	Q53020 r outer mem
25	166	5.5	1025	1 SLAP_CAUCR	P35828 caulobacter
26	165.5	5.5	1300	1 120K_RICRI	P14914 rickettsia
27	164.5	5.5	444	1 SLAP_LACAC	P35829 lactobacill
28	163	5.4	550	1 FLIC_SHIFL	Q08860 shigella fl
29	161.5	5.4	1637	1 MRSP_STRAU	P80544 staphylococ
30	159.5	5.3	642	1 FLID_CAMJE	Q9phw6 campylobact
31	159	5.3	671	1 Alys_ENTFA	P37710 enterococu
32	159	5.3	928	1 PM10_CHLPN	Q9rb65 chlamydia p
33	158	5.3	497	1 FLIC_ECOLI	P04949 escherichia

#### ALIGNMENTS

##### RESULT\_1

AG43\_ECOLI  
ID AG43\_ECOLI STANDARD; PRT; 1039 AA.  
AC P39180; P75614; P97241; Q46771;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (AG43) (Fluffing protein).  
GN FLU OR B2000.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,  
Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,  
Yamamoto Y., Horiuchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML 308-225;  
RX Henderson I.R., Owen P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP PRELIMINARY SEQUENCE OF 53-78.  
RC STRAIN=ML 308-225;  
RX MEDLINE=89291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN [5]  
RP SEQUENCE OF 53-63.  
RC STRAIN=K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded

in the genome of *Escherichia coli* K-12.;"

RL Electrophoresis 18:1259-1313(1997).

RN [6]

RX GENE NAME.

RA MEDLINE=97257509; PubMed=9103983;

RA Henderson I.R., Meehan M., Owen P.;

RA "Antigen 43, a phase-variable bipartite outer membrane protein,

RT determines colony morphology and autoaggregation in *Escherichia coli*

RT K-12.;"

RL FEMS Microbiol. Lett. 149:115-120(1997).

CC -!- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY

CC FUNCTION AS AN ADHESIN.

CC -!- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA

CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA

CC CHAIN).

CC -!- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.

CC -!- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETTELLA PERTACTIN.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; AE000291; AAC75061.1; ALT\_INIT.

DR EMBL; D90839; BAA15825.1; ALT\_INIT.

DR EMBL; D90839; BAA15832.1; ALT\_INIT.

DR EMBL; U24429; AAB47869.1; -.

DR EcoGene; EGI2686; flu.

KW Outer membrane; Signal; Complete proteome.

KW

FT SIGNAL 1 52

FT CHAIN 53 551

FT CHAIN 552 1039

FT ANTIGEN 43 ALPHA CHAIN.

FT K -> N (IN STRAIN ML 308-225).

FT SL -> FF (IN STRAIN ML 308-225).

FT T -> K (IN STRAIN ML 308-225).

FT W -> L (IN STRAIN ML 308-225).

FT V -> F (IN STRAIN ML 308-225).

FT ATN -> STI (IN STRAIN ML 308-225).

FT A -> T (IN STRAIN ML 308-225).

FT N -> Q (IN STRAIN ML 308-225).

FT E -> V (IN STRAIN ML 308-225).

FT S -> N (IN STRAIN ML 308-225).

FT H -> Y (IN STRAIN ML 308-225).

FT E -> K (IN STRAIN ML 308-225).

FT M -> T (IN STRAIN ML 308-225).

FT GHL -> SHF (IN STRAIN ML 308-225).

FT S -> P (IN STRAIN ML 308-225).

FT A -> V (IN STRAIN ML 308-225).

FT C -> S (IN STRAIN ML 308-225).

FT LNLVHTS -> MNLIYNA (IN STRAIN ML 308-225).

FT QGT -> LGA (IN STRAIN ML 308-225).

FT S -> T (IN STRAIN ML 308-225).

FT Q -> L (IN STRAIN ML 308-225).

FT S -> I (IN STRAIN ML 308-225).

FT ETV -> TTT (IN STRAIN ML 308-225).

FT

SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;

VARIANT 845 847

VARIANT 855 855

VARIANT 888 888

VARIANT 1025 1025

CONFLICT 61 63

SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;

Query Match

Best Local Similarity 7.8%; Score 235.5; DB 1; Length 1039;

Matches 144; Conservative 23.1%; Pred. No. 0.00014;

Mismatches 203; Indels 205; Gaps 35;

1 MNKTYRLVNSALNAAVAVSELTNRHKKASATVKATVATLLFATVQASANNEDQEDL 60

5 LNTCYRLVNNHMTGAFVNSALAKRGKGVAVLSLAIVSLPVLAA-----DI 55

61 YLDPVQRTVAVLVNSDKE---GTGEKEKEEENSNDWVFNKGVLTAREITLAKGNLKL 117

56 VHPGPEVNGGTLHNDQNVFGT----- 79

QY 118 IKONGTNFTYSLKKDLTDLTSTVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDFTV 177

DB 80 --TNGMTITSTGLEYPDNEANTGQWODGTANKTTVTSG--GLQ- RYNPGGSVSDTVI 134

QY 178 HLAGIGSTL---TDTLLNTG-----ATTNVTNDNVTDDKKRAASVKDVLNAGWN 224

DB 135 SAGG-GOSLQGRAVNTTLNGGQWHEGAIATGVINDK-----GWQ 175

QY 225 IKGVKPTTASNDVDFRT-----YDTVEFLSADTKTTTVNVESKDNKGKKEVKI 274

DB 176 V--VKPTVATDIV--VNTGABGGPDAENGDTGQFVRGDAVRTIN---KNGRQIVRAE 227

QY 275 G-AKTSVIREKDKLVTKGDKGSGSSPDE---GEGLV---TAKEVIDAVNKGAWRM- 324

DB 228 GTANTIVV-----YAGDQTVHGHALDTFLNGGYQYVHNGGTASDTV--VNSDGGWIV 278

QY 325 -----KTTTANGCQTQADKFTVTSNTVTFASG-----KGTATVSKDDQG-NITVMD 373

DB 279 KNGVAGNTTVN-OKGRL-OVDAGGTATNVLKOGGALVTSTAATVT-----GINRLGAFS 332

QY 374 VNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDETVNINANNIEITRN 433

DB 333 VVEGKADNV-VLENGG-RLD-----VLTGHTATN-----TRVDDGGTLDV-RN 372

QY 434 GKNIATSMTPQFSVSVISGAGADAPTLSDVDGALNVGSKKNPKVRITNVPAGKEGDV 493

DB 373 G-----GTATT-----VSMGNGG---VLLADSGAAVSGTRSDCK-----AFSIGGQA 412

QY 494 TNVAQLKGVAQNLNNRDNVDGNARAGIAQAIAITAGLVQAYLPKGSMAIGGTGVRGAG 553

DB 413 DALMLEKSGSFTLN-----AGDTATDTT-----VNGGLFTARGG 446

QY 554 YAIGYSISDGGNWIKGTASGN 576

DB 447 TLAGTTTLNNGAILTLGKTVNN 469

## RESULT 2

YDBA\_ECOLI STANDARD: PRT: 2003 AA.

ID P33656; P76087; P76088; P76856; P76857; P76859;

DT 01-FEB-1994 (Rel. 28, created)

DT 16-OCT-2001 (Rel. 40, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Hypothetical protein ydbA.

GN YDBA OR B1401/B1405.

OS *Escherichia coli*.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC *Escherichia*.

OX NCBI\_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of *Escherichia coli* K-12.;"

RL Science 277:1453-1474(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=K12.

RX MEDLINE=97251357; PubMed=9097039;

RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

RA Kesai H., Kishimoto K., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,

RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,

RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;

RT "A 570-Kb DNA sequence of the *Escherichia coli* K-12 genome

RT corresponding to the 28.0-40.1 min region on the linkage map.;"



```
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN-K12:
RA MEDLINE=92190338; PubMed=1665988;
RX Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
  Escherichia coli K-12.";
RT Biochimie 73:1361-1374(1991).
RL Biochimie 73:1361-1374(1991).
CC -I- SIMILARITY: TO S. TYPHIMURUM ORF NEAR CYSG (AC P25928).
CC -I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -: NOT ANNOTATED_CDS.
DR EcoGene; BGL1307; ydbA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 7.4%; Score 221; DB 1; Length 2003;
Best Local Similarity 23.6%; Pred. No. 0.0015;
Matches 167; Conservative 75; Mismatches 230; Indels 236; Gaps 40;

QY 50 SANNEEQEEDLYLPVQRTV---AVLVNSDKECT-----GEKEKV-----EENS 92
DB 141 SFNN-----DVLDKTEKTLTIRDSVFTYTNADGTISLQDSNGRKATINLWQIDEANNT 195

QY 93 WAV-----YFNEKGVLTAIREITLKAGDNLIKQNGTNTFTYSLKDLTDLTISVGT 141
DB 196 VALEGSADGATKQYNHNGELVI-----TGDNATVNNNG-----KTTVDGKDSGT 242

QY 142 E-----KLFSFANGKNVITSDT-----KG-----LNF 164
DB 243 EINGNNGKRVIODGLDVGSGGHGIDITGDSATVDNKGKMTVTDPESMGITQIDGDKRAIVNN 302

QY 165 AKETAGTNGDTTVHLNG-----IGSLTIDTLLATGATTNVDNDVDEKKRAASVKD 217
DB 303 EGESITNGGTGTQDGDATANNKGTVDGKDSGTGEINGNKKVIQD-----GDLD 356

QY 218 VLNAGWNKGVKPGTTASDNDVFRYDTVEF--LSADTKTTTVNVYESKD----- 265
DB 357 VSGGGHGI-DITGDSATVDNKGKMTVTDPESIGIQVDGQDAVVNNEGESAINGTGQTQI 415

QY 266 NGKKEVTKIGAKTSVKEKDKLVTKGD-KGENG-----SSTD 302
DB 416 NGDDATANNNGKTTV-----DGKDSGTGTETAGNNGKRVIODGLDVGSGGHGIDITGDSATV 471

QY 303 EGEGLVTAKE-----VIDA-----VNKAGWRMKTITANGOTQADKFEFTVSGTNVTAS 352
DB 472 DNKGKMTVTPESIGIQIDGDAIVNNEG-----ESTITNGGT-----TQINGNDAT-AN 521

QY 353 GRGTTATYSKDD-----QCNITVMYDVMVGDALNV-----NOLQNSGWN--LDSK-----A 396
DB 522 NSGKTTVDGKDSGTGKIAGNIGI---VNLDSGLTYTGAHGVENIGDNGTNNKGDIVVS 578

QY 397 VAGSSGKVIISGVNPSKGMDETVINAGNNIEIFTRNKNIDIAISM-TPOFS----- 448
DB 141 SFNN-----DVLDKTEKTLTIRDSVFTYTNADGTISLQDSNGRKATINLWQIDEANNT 195
```

```
DB 579 DTGSIGVLINGEGATVSNVTGDVNVNS-NEATGFSITTSCKVSLAGSMQVGFSTGVDLNG 637
QY 449 ---SVSLGA-----GADAPTLISVDGDALNV---CSKDKNKPVRITNVA-----PGV--- 488
DB 638 NNNSVTLAAKDLKVVQKATGINSGDANTVNITGNVLVDKDTADNAAEYFFDPSVGIN 697
QY 489 ---KEGDVTNVAQLKGVAQN-LNNRIDNV-DGNARAGIAQAATATAGLV----- 531
DB 698 VYGSNNVTLDGKLTVVSDSEVTSRQSNLFDGSAB-----KTSGLVVIGDGNVTNMG 750
QY 532 -QAYLPGKSMMAIGGTYRGAGYAI-----GYSSISDGDGNWIIKG 571
DB 751 GLELIGEKNALADGSQVTSRLRTGYSTYSVIVVSGESSVYLNGDITISG 798

RESULT 3
IDA_AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC Q03155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aidA-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Plasmid pIB6.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (O126:H27);
RX MEDLINE=92326638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
  diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
  synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -I- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -I- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X65022; CAA46156.1; -.
DR PIR; S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-I.
FT PROPEP ? 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 7.1%; Score 212.5; DB 1; Length 1286;
Best Local Similarity 21.1%; Pred. No. 0.0023;
Matches 144; Conservative 94; Mismatches 274; Indels 171; Gaps 29;

QY 1 MNKIYRITWNSALNAWAVSELTRNH-----TKRASATVKA--VLATLFLFATVQASA 51
DB 1 MNKAYSIIWHSRQAVIVASELARGHGFVLAKNTLLVLAVSTIGNAFVAVNSGTSSGG 60
QY 52 NNEEQEEDL-----YLDPVQRTVAVLVNSDKEGTGEKEKVEE---N 90
DB 61 TVSSGETQIVSYSGRNSNATVNSGGTQIVNNGKGTATTVNSGSONVSGTATSTIVN 120
QY 91 SDWAVYFNEKGVLTAIREIT-----LKAGDNLIKQNGTNTFTYSLK-KLTDLTLSVGT 141
```

```
Db 121 SGGIQRVSSGGVASATNLSSGAQNIYNLGHASNTVIFSGGNGTIDSTNISSGGQ 180
Qy 142 EKLFSFANGKNVITSDTKGLNFAKETAGTNGTIVHLN-----GIGSTLTDLTLLNTG 194
Db 181 QRV--SSGGVASNTTINS--AQNLSEGAISTHSSGGNQYISAGANATETIVNSG 235
Qy 195 ATTNVNDVNTDEKKRAASKVQVLNAGNIGKVRKPTASDNVDFVETDVTVEFLSADT 254
Db 236 GFORVNSG-----AVATGTVLSG--TQNVSSGSAISTSVNSGVQTV--FAGATV 283
Qy 255 KITTVNVESKDN---GKKTEVKIGAKTVIKEKDKGLVTKDKGKNGSSTDEGEGLVTA 310
Db 284 TDTVNSGNGNQISSGLVSETTVNSGTONIYSSGSAISANIKGS-----329
Qy 311 KEVIDAVNKGWRMKTITANG-----QTQADKQFETVSGTNVTFASG-----KGT 356
Db 330 ----QVNSGEGTAINTVSDGGYOHIRNGGIASGTIVNSQGVYNISSGVAESTIINS 385
Qy 357 TATVSKDQGNITVMYD---VNVGD-ALANVNOIQNSGWNL-----DSKAVAGSSG--K 403
Db 386 TLRVLSGTYARGTILNNSGRENVSNGGVSYNAMINTGGNQIYISDGEATAIIVTSGFOR 445
Qy 404 VISGNVSPSKGMDVETNINAGN---NIEITRNGKN-----IDIATSMTPQF 447
Db 446 INSGGTAPVONSVVVTRTSSAAKPDAEVYSGGKQTVLWRIWISNFLTAVWSMPCGT 505
Qy 448 SS---VSLGAGADAPTLSDVDGDLN-----VGSKKDKKPVRTINVPAGV 488
Db 506 ASGANVLSGRLNAGNVVGTILNQEGROYVYSGATATSVNNGEGREYV-----LSGGI 561
Qy 489 KEGDVTNVAQLKGAQNLNRRIDNVGNARA-----GTAQAIATAGLVQAYLPGKSMAL 543
Db 562 TDTVLSGGLQAVSSG-----GKASATVINEGGAQFYDGGQV-----TGTNIK-- 606
Qy 544 GGGTREGAGYAGVSSISDGGN 566
Db 607 NGGTIRVDSGASALNIALSSGGN 629

RESULT 4
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC F32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN Hypothetical lipoprotein ydek precursor (ORF7).
OS YDEK OR ORF7 OR B1510.
OC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Wu B., Shao Y.;
RT The complete genome sequence of Escherichia coli K-12.;
RL Science 277:1453-1474 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
```

```
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28,040,1 min region on the linkage map.";
RL DNA Res. 3:363-377 (1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cardright P.J., Tilms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347 (1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AE000248; AAC74583.1;
CC EMBL: D90793; BAA15190.1; ALT_INIT.
CC EMBL: D90794; BAA15197.1; ALT_INIT.
CC EMBL: X73295; CAA51730.1; ALT_FRAME.
CC PIR: S34315; S34315.
CC Ecogene: EGI1780; Ydek.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
CC Hypothetical protein; Membrane; Lipoprotein; Signal;
CC Complete proteome.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
CC LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
CC CONFLICT 884 M -> K (IN REF. 3).
CC CONFLICT 1317 1317 M -> S (IN REF. 3).
CC SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;
CC
CC Query Match 7.0%; Score 210; DB 1; Length 1325;
CC Best Local Similarity 22.9%; Pred. No. 0.0032;
CC Matches 148; Conservative 72; Mismatches 266; Indels 160; Gaps 27;
Qy 1 MNKIYRIWNSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEEL 60
Db 1 MNRIYRVINWCTLQVQACSELTRRAGKTSTVNLKSSGLTTKFSRL-----47
Qy 61 YLDPQRTVAVLVNSDKGTGKTEKKEKRENSDWAYFNEKGVLTAREITLKAGDNLKIKQ 120
Db 48 -----TLGVLLALS---GSASGASLEVDNDQI-----71
Qy 121 NGTFTVSLKKDLTDTLSVGTETKLSFANGKNVITSDTKGLNFAKETAGTNGTIVHLN 180
Db 72 --TNIDTVDAYDAYLVGVNWTGTVGLNLAGGN-ASLTITTSV-----IGANEDSEGTVN 122
Qy 181 GIGST--LTDV-----LLNTG-----ATTNVDNVDYDDEKKRAASKVQVLNAGNIGK 229
Db 123 VLGGTWRVLYDSGNARPLNVGSGGTGLNIKQKHVDG-----GYLRIGSGSGGV- 172
Qy 230 PGTTASDNVDVFRVTDYTFELFSADTKTTTVNVESKDKKTE-----VKIGAKTSVIK 282
Db 173 -GTNVNVEDGSVLTTELFEGSYGTGLNIT----DAGYVTSSIVAILGYQAGSNGQVV 227
Qy 283 EKDGK-LVTGKDKG-----ENGSSYDEGEGLVTAKEVIDAVNKGWRMKTITANGT 333
Db 228 EKGGEWLKKNDSIEFQIGNQGTGEATIREGGVLVTAENTIIIGNATG----IGTLNQQ- 282
Qy 334 GQADKFEETVSGTNVTFASGKGTGTATVSKDQGNITVMYDYNVNDGDLN--VNOIQNSGN 391
```

```
Db 283 -DQSVITVRLRYGFGNG---TVNISNGLINKEYSLVGVQDGSFGVNVVTDKGHW 338
Qy 392 L-----DSKAVAGSSGKVISGVNPSKKGWDET-----VNIN 423
Db 339 FLGTGEAPRYIYGADGELNVSEGVKVDGSIITAG---MKETGTGNTITVKDKNSVITN 395
Qy 424 AGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGDLNVGSKKD-NKPVRIIT 482
Db 396 LGTNLGYDGHGEMNINISNOGLVSVNGGSSLYGX----ETGVGNVSITTTGGMWEVKNVYTT 451
Qy 483 NVAPGVKEGDTNVVAQLKGVQNLNRRIDNVGNARAGIAQIATAGLVQAYLP--GKSM 540
Db 452 IGAVAGVGNLNSDGG--KEVSQNTIFLGDKASGIGTGLNMDATSSFDTVGINVGFGSGI 509
Qy 541 MAIGGTYVRGEAYAI-----GYSSISDGGNWIIGKTASGNSR 578
Db 510 VNVSNGLNTSTGYGFIGGNASGKIVNISTDSLNLNA--TSSTNAQ 554

RESULT 5
HLXA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S. MARCESCENS HEMOLYSIN (SHLA).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30186; AAA25657.1; -.
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
```

Query Match 6.9%; Score 207.5; DB 1; Length 1577;  
Best Local Similarity 22.3%; Pred. No. 0.0052;  
Matches 154; Conservative 86; Mismatches 258; Indels 193; Gaps 32;

```
Qy 22 LTRNHTKRASATVKTAVLATLFLATVQASANNEQEEEDLYDPVQRTVAVLIVNSDK--- 78
Db 306 ITVNNSSGSSQTLTKTELAKNI--TLVASSHQIKASDLMDGDDITLQGLDQKQLOQ 363
Qy 79 -----EGTGEKEKVE-----ENSDWAVYFNEKGVLTAREITLKAGDNLK 117
Db 364 KETDIDNRFYSWKYDVTKEKEQIQIGSQIDAKNNATLTATKGDVTLDAAKINAGNNLA 423
Qy 118 IKONCTNFTYSLKKDLTDLTSVG-TEKLSFSANGKNVNITS-----DTKGLNFA 165
Db 424 INAN-----KDIHINGLVEKESRSENGKRRHTSRLSESGSWSNSHQETFLKAS 471
Qy 166 KETAG-----TNGDITVHLN-----GIGSTLTDLL---NT 193
Db 472 ELTAGKDLGLDAQSITAGAKLHANENVLVNAKNINLVQKTNNDKTTVTNHHVMWGI 531
Qy 194 GATTNVTNDN-----VTDDEKKRAASVKDVLNAGNINIG-----VKPOTTSADNVD 239
Db 532 GGGQKNNNNOOVSHATQLTADGQLLAAADNNVNITGSQVKNGQGAFFK--TTQGDVVI 589
Qy 240 FVRTYDTVEFLSAD-----TKTTTVNVESKDCKKTEVKIGAKTSVKEKD----GKL 288
Db 590 DNALSETISKIDERTGTAENITKSKHKNETNKQTSTGSELISDAQLTVVSGNDVNVIGSL 649
Qy 289 VTGDKD-----GE-NGSST-----DEGEGLVT---AKEVIDAVNKAGWRKTTTANG 331
Db 650 IKSADKLGHSGLDINVKSAQOQVTKIDDEKTSIAITGHAKEVEDKQYSAGPHITHTNKN 709
Qy 332 QTGQADKFTVTSYGTNVTFAASKGTATVVS--KDDGQNTVMYDVNVGDALNVNQLNSG 389
Db 710 TSTETEQAQNSTISGANVDLQANKDVTFAGSLKTTAGNASITGD-NVAFVSTENKKQTD- 767
Qy 390 WNLDKAVAGSSGKVISGVNPSKGMDETNNINAGNNIEITRN-GKNIDIASITPQPS 448
Db 768 -NTDTTISGGFS---YTGVDKVGSKADFOYD-KOHTQTEVTKNRGSETEVAGDLTITAN 822
Qy 449 SVSLGAGA-----DAPTLSDGDLNVGSKKD-----NKPV 479
Db 823 KDLLHEGASHHVEGRYQESGENIQHLAVNDSEKST--DSLNVGIDGVNLDYSGVTRPV 880
Qy 480 R-----TTNVAPGVKEGDTNVVAQLKGVQNLNRRIDNVGNARAGIAQIATAGLVQA 533
Db 881 KKAIEDGVNTTKPG-NTTDLTKKVTARDAIANLAN-LSNLE-TPNVGVEVGK----- 930
Qy 534 YLPGRKMAIGGTYVRGEAYAI GYSSISD 564
Db 931 -----GGGSOQSQTDSOAVSTISINAG 951

RESULT 6
OMP_RICRI
ID OMPB RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame;
RT evidence for protein processing from a large precursor.";
```

RL Mol. Microbiol. 5:2361-2370(1991).  
 RN [2]  
 RP SEQUENCE OF 279-1654 FROM N.A.  
 RC STRAIN-R;  
 RX MEDLINE=50136087; PubMed=2515418;  
 RA Gilmore R.D. Jr. Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the  
 RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X16353; CAA34403.1;  
 DR InterPro: IPR003858; rOmpA\_rOmpB.  
 DR Pfam: PF02708; rOmpA\_rOmpB.1.  
 KW Antigen; S-layer; Cell wall.  
 FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.  
 FT DOMAIN 1181 1188 POLY-THR.  
 FT SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;  
 SQ

Query Match 6.7%; Score 201; DB 1; Length 1654;  
 Best Local Similarity 22.6%; Pred. No. 0.011;  
 Matches 164; Conservative 83; Mismatches 282; Indels 196; Gaps 33;

QY 7 IUNSLNNAWAVSELTR-----NHTKRASATVKTAVLATLFAVQASAN 52  
 DB 92 LLTANNALVTSDETLTGFTTNVHNSFNLNAG---KLTITGQGVNAQAAT 148  
 QY 53 NEFQEDLYDPQRTAVLVINSDEKGEKEVEENSDMAVYFNEKGLTAREITLKA 112  
 DB 149 KNAQNV-----VYQFNNGAAIDNNDLKGVG---RIDFGAPASTLVNLANPTTOKAPLIL 200  
 QY 113 GDNLIKQNGTFTYSLKKDLTDLT--SVGTEKLSFANGKVNITSDTKLNFPAKETAG 170  
 DB 201 GDNVAVI-ANGVNGTLNVNGFIQVSNKSFATVKAINIADGQGIIFNTDANNANLNLQA- 258  
 QY 171 TNGDTTVHLNGIGSTLTDLTLLTGATNTVNDVNDDEKRAASKVDVLNAGWNKGVKP 230  
 DB 259 --GGTTINFTGDTGRLVLLSKHAA--ATNFNITG-----SLGGLKGVIE 301  
 QY 231 GTTASDNDVFRVTDYTFEFLSADTKTTTVN-----VESKDNGKKEV--KIGAKTSV 280  
 DB 302 FNTVA-----VDQLTANAGAAVIGTNGAGRAAGFVVDNGKVAITDQVYAKDMV 356  
 QY 281 IKEKCKLVTKG-----DKGENGS-----STDGEGGLTAKAVI 314  
 DB 357 IQSAN--ATGQVNRHIVDVGADCTTAFKTAASKVTITQDSNFGNTDFG--NLAQIKVP 412  
 QY 315 DAV-----NKAGRMKTTTANG--QTQADKFTVTSIGNVTFASGKGT-- 356  
 DB 413 NATLTGNTGDSNPGNTAG--VITFDANGTLLESASADANVAVTNNTITALEAGAGVQV 470  
 QY 357 -----TATVSKDDQGNITVYDVGNDALN--VNLQNSGWNWLSKAVAGSSGKVTSGNV 409  
 DB 471 LSTHAELRLNAGSIFPLAD---GTVINGKVNQYALVGGALAGTITLDGSAITIGDI 527  
 QY 410 SPKSGKM-----DETVNINA--GNNIETIRNGKNI-----D 438  
 DB 528 GNAGGAALQRTLLANDAKKTLTLLGANAIIAGGGTIDILQANGGTIKILTSTQNNVIVDFD 587

QY 439 IATSMTPQFSSVSLGAGADAPTLSDVG-----DALNVSKK---DNKPVPRITN 483  
 DB 588 LAIA-TDQGVVDASSLTNAQTLLTKGKGTGANNKTLGQPNIGSKSTVLSNGVAIN 646  
 QY 484 VAPGVKEGDV-----TNVAQLGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQAY 534  
 DB 647 LVIG-NDGAVQFAHDTYLLTRTTNAAQGGKLIIFNPVNVNGTTTLAGNLSATNPLAEIN 705  
 QY 535 LPCK-----SMAIGGGTYRGEAGYA-----IGYSSISDGGNNIIKGTASGNSRGH 580  
 DB 706 FSGKGVNDVTVLNVGEGVNL-----YATNITTTDANVGSFVNAGTIVSGTVGGQGNK 761  
 QY 581 FGASA 585  
 DB 762 FNTVA 766

RESULT 7  
 ID HLVA\_SERMA STANDARD; PRT; 1608 AA.  
 AC P15320;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Hemolysin precursor.  
 GN SHLA.  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
 RC STRAIN-SN8;  
 RX MEDLINE=88257037; PubMed=3290200;  
 RA Poole K., Schiebel E., Braun V.;  
 RT "Molecular characterization of the hemolysin determinant of Serratia  
 RT marcescens.";  
 RL J. Bacteriol. 170:3177-3188(1988).  
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
 CC DEFINED.  
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
 CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
 CC REQUIRES SHLB FUNCTION.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane.  
 CC -1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M22618; AAA50323.1;  
 DR PIR: A28182; A28182.  
 KW Hemolysin; Toxin; Outer membrane; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 1608 HEMOLYSIN.  
 SQ SEQUENCE 1608 AA; 165078 MW; D669B476F7DAD51 CRC64;

Query Match 6.4%; Score 191.5; DB 1; Length 1608;  
 Best Local Similarity 21.8%; Pred. No. 0.032;  
 Matches 151; Conservative 87; Mismatches 239; Indels 217; Gaps 34;  
 QY 24 RNHTKR-----ASATVKTAVALTLATLFAVQASANNEEQ-----BEDLYLDP--- 64  
 DB 460 RNHTSSLTGRWSNDESELSKASERSEGLTLKAGRNVTQGAQVHAQRLDTIDADNO 519  
 QY 65 ----VQRTVAVLVNSDKGTGKVEKVEENSDMAVYFNEKGLTAREITLKAQDNLIKQ 120

```
Db 520 IQVGQKATANAKAVRDDTSWG-----GIGGDN---K 549
Qy 121 NCTNFTYSIKDL---TDLTSVGTTEKLSFANGNK-VNIT-SDTKGLNFAKETAGTNGDT 175
Db 550 NNSN-----RREISHASELTSGLTURL-----NGQGVTITGSKARGQGEVTA-THGGL 599
Qy 176 TVHLNGIGSTLDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIRKVKPGTTAS 235
Db 600 RID-NALSTTVDKIDARTGTAFNITSSSHKADNSVQSSTASEL-----KSD 644
Qy 236 DNVDFVRYDYVEF-----LSADTKTTTVNVE----- 262
Db 645 TNLTLVSHKDAVDIGSVASGELSVESTKGINVKAEROQNIDEQKTALTIVNGYAKEA 704
Qy 263 -----SKDNCKTEVKIGAKTSYIKEDGKLVTKCKGKENGSS--TDEGEL 307
Db 705 GDKQVRAGLRIEHTRDSEKTRTNSA---SSLSGGSVKLKAEDVTFSGSKLVADKGDAS 762
Qy 308 VTAKEV--IDAVNKAGRMKTTTANG---QTQADKFETVTSCTNVTFSAGKGTATTATVSK 362
Db 763 VSGNKVSFLAADDKTASWTEQTKIGGFYTTGGIDK---LGSVGEAGYENNK-TQAQSK 818
Qy 363 -----DQGNITVMDVNVGDALNVQLNSGNWLDKSAVAGSSGKVISGNVSPSKGM 416
Db 819 AITSGSDVKGNLT-----INARDKLTQQAQHSVGGAYQENAGVDHAAADTASTTTTKT 874
Qy 417 DETVNINAGNLEITRNKNIDTATSMTPQFSSVSLGA-----GADATLSVD 464
Db 875 DVGWNI-----GANVDYSAVTRPVERAVRGAAKLADATGVIINDIGGIGAPNVGLD 923
Qy 465 GDALNVGSKK--DNKPVRTITNAPGV---KEGDV---TNVAQLKGVAQNLN----- 507
Db 924 IGAQGSSEKSSSSQAVSVSSVQAGSIDINAKGEVRODGTQYQASKG-AVNLTADSHRSE 982
Qy 508 ---NRIDVNGNARAGIAQAATAGLVQAYLPKGSMAIG---CGTYRGEAGYAIYGSS 560
Db 983 AAANRQDEQSRDR-----GSAG-VRVYTTTGSDLVADKAGEGQTORSNSSASQAVTG 1034
Qy 561 ISDGNW-----IIKTASGNSRGHFGASA 585
Db 1035 SIDAANGINNVKKDAIYOGTALNGRGRKTAVNA 1068

RESULT 8
OMPA_RICRI STANDARD; PRT: 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
DE antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
RT repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- PTM: GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSTAE OMPA/OMP B FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
```

```
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31227; AAA26380.1; -.
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; s-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE I).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D5646C089DF087 CRC64;

Query Match 6.4%; Score 191; DB 1; Length 2249;
Best Local Similarity 24.4%; Pred. No. 0.051;
Matches 142; Conservative 56; Mismatches 212; Indels 172; Gaps 30;

Qy 98 NEKGVLTAIREITLKAGDNLKIKQNGTNTFTYSLKK---DLTDLTSVTEKLSFSAN---G 150
Db 766 NANAVLTGAIDNTTGGDNVGV---LNLNGALSQVTDGIDGNTNSLAT--ISVGAGTATG 819
Qy 151 NKVNITSQTKGLNFAKETAGTN-----GDT--TVHLNGIGSTLTDLLNT- 193
Db 820 GAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTGGDNVGVNLNLNGALSQVTDGIDGNTN 879
Qy 194 -----GATTNVTNDVNTDDEKRAASVKDVLNAGWNIRKVKPGTTASDNV 238
Db 880 SLATISVGAGTATLGGAVIKATTTKLTN-----AASVLTNANAVLTGAIDNTTGGDNV 934
Qy 239 DFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVIGAKTSVKEKDGKLVTKCKGKENG 298
Db 935 GVLNLNGALSQVTDGIDNT-----NSLAT-ISVGAGTATL----- 968
Qy 299 SSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGQTQADKFETVTSCTNVTFSAGKGTTA 358
Db 969 -----GGAVIKATTTKLTDAASAVKFTNPPVVTGAIIDNTGNANNGI-VTFGTNSTVVG 1020
Qy 359 TVSKDDQGNITVMYDYNVGDALNVQLNSGNWLDKSAVAGSSGKVISGNVSPSKGMDE 418
Db 1021 NV-----GNTNALATVNVGAGL--LOVQGVVKVANKINITDNASAVTFTNPPVVTGAIIDN 1073
Qy 419 TVNINAG-----NNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDAL--NVG 471
Db 1074 TGNANNGIVTFGTNSTVTVGNVGN-----TNALATVNVGAG-----LLQVQGVVKANT 1122
Qy 472 SKKDN-KPVRTNVPAGVKEGVDVTVNVQALKGVAQNLNINRDNVDGNARA-----GTAQATA 526
Db 1123 NLTDNASAVTFTN--PPVVTGAIIDNTG-----NANNGIVTFGTNSTVTVGIDGNTNALA 1173
Qy 527 T----AGL-VQAYLPCKSMMA-----IGSGTYRGEAGYAIYG---SSIS 562
Db 1174 TVNVGAGITLQA---GGSLLAANNIDFGARSTLEFNGLDGG-----GRAIPYFKGATA 1224
Qy 563 DGGNMIK-----GTASGNSRGH---FGASASVG 588
```



GN OMPB OR RCI085.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OX Rickettsiaceae; Rickettsieae; Rickettsia.  
NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RS Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
RL Science 293:2093-2098(2001).  
RN [2]  
RP SEQUENCE OF 33-1649 FROM N.A.  
RC STRAIN=Indian tick typhus, and Malish 7;  
RX MEDLINE=20393643; PubMed=10939649;  
RA Roux V., Raoult D.;  
RT "Phylogenetic analysis of members of the genus Rickettsia using the  
RL gene coding the outer-membrane protein rOmpB (ompB).";  
RN Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).  
RN [3]  
RP SEQUENCE OF 353-1655 FROM N.A.  
RC STRAIN=Malish 7;  
RA Stenos J., Walker D.;  
RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
RL australis, the most divergent rickettsia of the spotted fever group.";  
RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
CC SIMILARITY).  
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
CC (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC -----  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AE008659; AAL03623.1; -;  
DR EMBL; AF123721; AAF34124.1; -;  
DR EMBL; AF123726; AAF34129.1; -;  
DR EMBL; AF149110; AAD39533.1; -;  
DR InterPro: IPR003858; rOmpA\_rOmpB.  
DR Pfam: PF02708; rOmpA\_rOmpB;  
KW Antigen; S-layer; Cell wall; Complete proteome.  
FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.  
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 353 354 KD -> GH (IN REF. 3).  
FT CONFLICT 776 776 F -> S (IN REF. 3).  
FT CONFLICT 1159 1159 E -> D (IN REF. 3).  
FT CONFLICT 1177 1177 G -> S (IN REF. 3).  
FT CONFLICT 1492 1492 H -> R (IN REF. 3).  
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match

6.2%; Score 186.5; DB 1; Length 1655;

Best Local Similarity 21.6%; Pred. No. 0.058;  
Matches 161; Conservative 77; Mismatches 266; Indels 241; Gaps 36;  
QY 10 NSALANWAVASELT-----RNHTKASATVKTAVLATLLPATVQASANNEQEE 58  
DB 95 NFNALNDVTVRREDTTLGFTTNVNNANHNLNAGKTLTTTGGGINTVQAAATKANNV 154  
QY 59 DLYLDPQVQRTVAVLIVNSDKEGTGEKEKVEENSQWAVYENKGVLTAREITLKAGDNLKI 118  
DB 155 -----VAQVNNCAAIDNDLOGVGRIDCGAAS--TLVFNLANP-TTKAPLILGDNAVI 206  
QY 119 KONGNFYSLKKDLTDLTSVTEKLSFSAKNGKVNITSDTKGLNFAKETAQTN----- 172  
DB 207 -VNGANGTLNVNTNGFIKVS-----KSF-ATVNVINI-GDGGGINFNTDADNVNTLNQA 258  
QY 173 GDTTVHLNIGIGSTLTDLLNTGATNTVNDVNTDDEKKRAASVKDVLNAGWNKVKPCT 232  
DB 259 NGATITFNGTDGTGRLLVLSKNA--ATDFNVTG-----SUGGNLKG1----- 299  
QY 233 TASDNVDFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIEKDKGLVTGK 292  
DB 300 -----IEF-----NTVAVNGOLKANA-----GANAIVIGTNG---AGR 330  
QY 293 DKG-----ENG-S-STDEGE-----GLVTAKEVIDAVNKAGWRMKT----- 327  
DB 331 AAGFVSVVDNGKVATIDGOVYAKDMVIOQANAVGVNFRHIVDVGTDGTTAFKTAASKVA 390  
QY 328 -TANGOTQADRF-----EIVTSGTNTV-FASGKGTTA-TVSKDDQNI-TVMYD 373  
DB 391 ITQNSNFGTID-FGNLAAQIIVPNTMTLNGNFTGASNPGNTAGVITFDANGLASASAD 449  
QY 374 VNVGDALNVNQLQNSGWNLDKA-----VAGS-----SGKVISGVNSPSK----- 413  
DB 450 ANVAVTNITAEASGAGVQVLSGTHAELRLGNAGSVFKLADGTIVNGKVQALVGGA 509  
QY 414 -----GKMDTETVNI----- 424  
DB 510 LAAGTITLDSATITGIDGNAGGAALOGITLANDATKTLTGGANIIGANGTINFAQN 569  
QY 425 GNNIETTRNGKI---DIATSMTPQFSVSLGAGADAPTLSDGDLANVGSKKDNKPYR 480  
DB 570 GTITLSTQNNIVDFDUAIA-TDQTVVDASSLTNAQTLTINGKIGTVGA--NNKTUG 626  
QY 481 ITNVAPG---VKEGDV-----TNVAQLKGVAQNLNRRINDVDC 515  
DB 627 QFNIGSSKTVLSDGDVAINELVIGNGVAQFAHNTYLITRTTNAAGQGKIIFNPVNNNT 686  
QY 516 NARAGIAQAIATAGLVQAYLPK-----SMAIIGGTYRGEAGYA-----IGYSS 560  
DB 687 TLATGTNLGSATNPLAEINFGSKGAANVDTVLNVG-----KGVNLATNTTTDANVGSFI 742  
QY 561 ISDGGNWIILKGTASGNSRCHFGASA 585  
DB 743 FNAGGTNIIVSGTVGGQGNKFNNTVA 767  
RESULT 11  
OMPB\_RICTY STANDARD; PRT; 1645 AA.  
ID OMPB\_RICTY  
AC P96989;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)  
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
GN OMPB OR SLP.  
OS Rickettsia typhi.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OX Rickettsiaceae; Rickettsieae; Rickettsia.  
NCBI\_TaxID=785;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-WILMINGTON;  
RA MEDLINE=94040787; PubMed=8224886;  
RX Hahn W.-J., Kim K.-K., Kim I., Chang W.-H.;  
RT "Cloning and sequence analysis of the gene encoding the crystalline  
RL surface layer protein of Rickettsia typhi.";  
RN Gene 133:129-133(1993).  
RP PARTIAL SEQUENCE.  
RC STRAIN-WILMINGTON;  
RX MEDLINE=92114896; PubMed=1370573;  
RA Chang W.M., Carl M., Dasch G.A.;  
RT "Mapping of monoclonal antibody binding sites on CNBR fragments of  
RL the S-layer protein antigens of Rickettsia typhi and Rickettsia  
RN prowazekii.";  
RM Mol. Immunol. 29:95-105(1992).  
RN [3]  
RP IDENTIFICATION OF CLEAVAGE SITE.  
RX MEDLINE=92104668; PubMed=1729180;  
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;  
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer  
RL membrane protein of Rickettsia: identification of an avirulent  
RN mutant deficient in processing.";  
RM Infect. Immun. 60:159-165(1992).  
RN [3]  
RP FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
RX STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
RA VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
RT "FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
RL S-LAYER WITH HEXAGONAL SYMMETRY. THIS BACTERIUM IS COVERED BY A  
RN SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY."  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L04661; AAB48987.1; -;  
DR InterPro; IPR003858; rOmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.  
KW Antigen; S-layer; Transmembrane; Cell wall.  
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
FT TRANSMEM 1354 1645 32 KDA BETA PEPTIDE.  
FT CHAIN 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
FT TRANSMEM 1415 1429 H -> N (IN REF. 2).  
FT CONFLICT 657 657 V -> I (IN REF. 2).  
FT CONFLICT 842 842 G -> A (IN REF. 2).  
FT CONFLICT 1071 1071 G -> S (IN REF. 2).  
FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;  
  
Query Match 6.2%; Score 185; DB 1; Length 1645;  
Best Local Similarity 21.5%; Pred. No. 0.068;  
Matches 164; Conservative 81; Mismatches 263; Indels 254; Gaps 40;  
  
QY 25 NHTKRASATV-----KTAVLATLLFAT---VOASANN-----EQEEDLYLDPV-- 65  
DB 40 NRTTAAATTVGAGDQFGAGVNLPAVATNSVITANSNAITPTNPNGLNLSFLDTANT 99  
QY 66 -----QRTVAVLIVNSDKG-----TGEKEVEE-----N 90  
DB 100 LAVTINENTTLGFTVNTVTKQGNFFNTIGAGKSLTITGHGITAQAATTKSAQNVSXV 159  
QY 91 SDNAVFPNE-KGV-----LTAREITLKAGNLKIKONGTNYFTYSLKK 131  
DB 160 AGAAINDNLSGVSGSIDFTAAPSVLEFNLINPTTQEAPLTLGDNAKI-VNGANGILNITN 218  
QY 132 ---DLTDLTSVGTKEKLSFAN-GNKVNITSD-TKGLNFAKETAGTNGDTTVHLNIGISTL 186  
DB 219 GFVKVSDKTFAGIKTIINIGDNOGLMNTTTPDAANLNL-----QGGGNTINFNRDGG-- 270

QY 187 TDTLLTNGATNTVNTDNVTDDEKKRAASVKVVLNAGNKGIV-RPGTTA----- 234  
DB 271 TGLVLVSKNGNATEFNVTG-----SLGGNLKGVIEFTDTTAAAGKLIANGGA 317  
QY 235 -----SDN-----VDFVRYDTVEFLSADTKTTTVNVYESKD-----NGKKT----- 270  
DB 318 ANAVIGTDNGAGRAAGFIVSVD-----NGNAATISGOVYAKDIVIQSANAGGQVTFEHLV 372  
QY 271 EVKIGAKTSVKEKDGKLVTKGDKGENGS--STDEG-----EGLVTAKEVIDAVN 318  
DB 373 DVGLGGKTN-FKTADSKVII---TENASFGSTDFGNLAVQIVVPPNNKILITGNFIGDAKN 427  
QY 319 K---AGWRMKTTTANGQ--TGQADKPEVTIS-----GTNVTFASG-----KGTAT 359  
DB 428 NGNTAG--VITFNANGTLVSGNTDPNVVITNIKAIEVEGAGIVQLSGIHGAELRLNAGS 485  
QY 360 YSKDOGNIITVMDVNVGDALNVNOLNSGNLSDSKAVAGSSGKVISGNSPSKGMDET 419  
DB 486 IFKLADGTV-INGPVNQNPPLVNNALAGSIQDGSAIL--TGDI--GNCVAVNAALQDIT 540  
QY 420 -----VNTNAGNNIEITPENGKNIDIAISM-----TPOFSSYS 451  
DB 541 LANDASKILLTSGANIIGANAGATHFQANGTQLTSTQNNILVDFDLDTDTQGVVD 600  
QY 452 LGACADAPTLSDVGD-----ALNVGSKK-----DNKPVRIIP- 482  
DB 601 ASSLTNQITINGSIGTGANKTKLGRPNVSGSKTILNAGDVAINELVMENDGVSVHLTH 660  
QY 483 NVAPGVKEGDTNVVQALKGVAQNLNNDVNGNARAGIAQAIATAGLVAQYLPKGSKMA 542  
DB 661 NYLITITINAAOGLIIVAAOPINTDTALADGTNLGSAESPLSNHIFATKAAGDSILH 720  
QY 543 IGGTYRGEAGYA-----IGYSSISDGGNNIIRGTAGS 575  
DB 721 IG-----KGVNLYANNITTTDANVWSLHFRSGTISVSGTVGG 758  
  
RESULT 12  
Y741\_CHLMU  
ID Y741\_CHLMU STANDARD; PRT: 1007 AA.  
AC Q9PJTG;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein TC0741 precursor.  
GN TC0741  
OS Chlamydia muridarum.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83560;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MoPn / Nigg;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
RT pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
CC -!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----



```
DR EMBL; AE002342; AAF39550.1; -.
DR TIGR; TC0741; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 51 POTENTIAL.
FT CHAIN 52 1007 HYPOTHETICAL PROTEIN TC0741.
SQ SEQUENCE 1007 AA; 104006 MW; 842800C0871B1518 CRC64;

Query Match
Best Local Similarity 21.5%; Score 183; DB 1; Length 1007;
Matches 156; Conservative 85; Mismatches 238; Indels 248; Gaps 38;

QY 31 SATVTAVLATLLFATVOASANNESQEDLYLDPVQRTVAVILVNSD----- 77
Db 227 SPTDKSSLLAFL--SNPNTKAKMLEHSHGLVFIDTTRSFIEVPNGDMVDCSMKVQNGK 284
QY 78 -KEGTGEKEKVEE-----NSDWAVYFNEKGVLTAREITLKAGDNL----- 116
Db 285 TKEDLGLKD-LEDCAKFCGTGYNKFSSDMG---NRVDPVLVSSKAGIESGGHLPSSVIINN 340
QY 117 -----KIKONGTNFTVSL--KKDLTDLTSV--GTEKLSFSANGKNV--ITS 157
Db 341 KFTCVAYCPNPKENPNYTSAMRHRVDFGKIFDGT-----APFNKINWSSPTP 394
QY 158 DFKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGAT-TNVTNDNVTDDEKKRAASVK 216
Db 395 GDDGISFSNETIGSEFPATPPSPSQTPVINVNVGTVNIGTNTVS----- 443
QY 217 DVLNAGWNLKVKPGT-TASDNVDFVRYDVFELSAADTKT---TVNVESKDNKKTEV 272
Db 444 -----KG--SGTPSSQSVDM--SDTSDLDTSIDTNTQNTNGDINTNDNNVDG 490
QY 273 KIGAKTSVIKEKDG---KLVTGDKD-----GNG 298
Db 491 SLSDVDSRVDDDDGVSDFSTNGDSGKTTSTENGDPGPDILAAVRKHLDTVPGENG 550
QY 299 STDDEGLVTAKE----VIDAVNAGWRMKTTHANGQTQADKFTETVTSNTVTFASGK 354
Db 551 GST---EGPLPANQLGNVHDEVEQNGSAKETIITPGDTGPTDSSSSVDADADVEDTS-- 605
QY 355 GTATVSKDDQGNITVMVDVNVGDALNVQLNSGNWLDKAVAGSSGKVI----- 405
Db 606 DTDSGIGDDDD-----GVSDTESTNG--NNSGKTTSTENGDPGPDILAAVRKHL 654
QY 406 ----SGNVSPSKGKMDETVINAGNNI-EITRNGKNIDIATSWTP-----QFSSVSLGAG 455
Db 655 TVYPGENGSTSEGL--PANQLNGVNHDEVEQNGAAQE--TIITPGDTESTDTSNVAN 710
QY 456 ADAPTL-----VDGDLNVGSKKDNKPV-----RITNVAP 486
Db 711 ADLEDVSDADSGFDDDDGIDSTESTNGDSGKNTPVGDGTPSGPDILAAVRKHLDTVP 770
QY 487 GYKEGDVTVNAQLKGAQNLLNRIDNVGNA-----RAGTAQATATAGLVOAYLP 536
Db 771 GENGSGTERPLPAN---QNLGDIHDEVEQNGSAKETVTVSPYRGGGNTSSPIGLA-SLLP 826
QY 537 -----GK-----SMAJGGGTYRGEAGYAIGYSSISDGGNWIIGTAS---- 574
Db 827 ATPSTPLMTPTNCKAAASLMIKGETQA-----KLKNGGN--IPGETTLAEL 875
QY 575 -GNSRGH 580
Db 876 LPLRGRH 882

RESULT 13
ID HXA3_HAEIN STANDARD; PRT; 917 AA.
AC P45355;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
```

```
protein A).
GN HXA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTHI N182;
RX MEDLINE=95115556; PubMed=7815944;
RA Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
  Mueller-Eberhard U., Hansen E.J.;
RT "The 100 kDa haem:haemopexin-binding protein of Haemophilus
  influenzae: structure and localization.";
RL Mol. Microbiol. 13:863-873(1994).
CC -!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation
  at the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U08349; AAA74139.1; -.
KW Transport; Signal; Repeat.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 917 HEME/HEMOPEXIN-BINDING PROTEIN.
FT DOMAIN 24 38 3 X 5 AA TANDEM REPEATS.
FT REPEAT 24 28 1-1.
FT REPEAT 29 33 1-2.
FT REPEAT 34 38 1-3.
FT DOMAIN 111 668 6 X 6 AA APPROXIMATE REPEATS.
FT REPEAT 111 116 2-1.
FT REPEAT 203 208 2-2.
FT REPEAT 277 282 2-3.
FT REPEAT 399 404 2-4.
FT REPEAT 624 629 2-5.
FT REPEAT 663 668 2-6.
FT DOMAIN 159 170 2 X 6 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 159 164 3-1.
FT REPEAT 165 170 3-2.
SQ SEQUENCE 917 AA; 100148 MW; 7FF39BB8C046539D CRC64;

Query Match
Best Local Similarity 6.1%; Score 182; DB 1; Length 917;
Matches 119; Conservative 92; Mismatches 223; Indels 124; Gaps 23;

QY 65 VORTVAVLIVNSDKEGTGEKEVE--ENSDWAVYFNEKGVLTAREITLKAGDNLKI---K 119
Db 59 INQTSKQVQINWHSFDIGQONKEVEFKQPSSENSVAYNRVTGGNASQIQGKLTANGKYYLAN 118
QY 120 QNGTNTYTSKDKDLTDLTSVGTSEKLSFSANGKNVITSDTKGLNFAKETAGTN-----GD 174
Db 119 PNGVIITKCAEINVAGLLATTKDLEQISENSNSYQFTRKTKDQVVKQGVNEGEIKAK 178
QY 175 TVVHLNGIGSTLTDLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNINIKGVKPGTTA 234
Db 179 DFVWLG-----DEVINKG-----NINV---EKNSTINGKVYLSSGYNFT-----FTL 218
QY 235 SDNVDFVRYDVFELSAADTKTTVN--VESKDNKKTEVKICAK----- 277
Db 219 SDS-----GISVALEDNTVRGIVONEGSKAGEITLSAKGRKALDSLVNMNV 267
QY 278 --TSVIKEKDKGLVTGKDKGE--NGSSTDEGEGLVTAKEVIDAVNAGWRMKTTHANGQ 334
Db 268 LEATKVSNGKGVLSADNVQLNNSNINKEIVNFGTEVTSNEDK---KLKITSKTGSKV 324
QY 335 QADKFTETVTSNTVTFASGKGTATVSKDDQGNITVMVDVNVGDALNVQLN-SGWNLD 393
Db 335 QADKFTETVTSNTVTFASGKGTATVSKDDQGNITVMVDVNVGDALNVQLN-SGWNLD 393
```



RA Mueller-Eberhard U., Hansen E.J.;  
RT "The 100 kDa haem:haemopexin-binding protein of Haemophilus  
RN influenzae: structure and localization";  
RL Mol. Microbiol. 13:863-873(1994).  
RN [2].  
RP SEQUENCE OF 1-30 FROM N.A.  
RC STRAIN-DL42 / SEROTYPE B;  
RX MEDLINE=95270579; PubMed=7751272;  
RT Cope L.D., Yovev R., Mueller-Eberhard U., Hansen E.J.;  
RA "A gene cluster involved in the utilization of both free heme and  
RT heme:haemopexin by Haemophilus influenzae type b";  
RL J. Bacteriol. 177:2644-2653(1995).  
CC -!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U08348; AAA74138.1; -.  
KW Transport; Signal; Repeat.  
FT SIGNAL 1 21  
FT CHAIN 22 928 HEME/HEMOPEXIN-BINDING PROTEIN.  
FT DOMAIN 101 679 6 X 6 AA APPROXIMATE REPEATS.  
FT REPEAT 101 106 1-1.  
FT REPEAT 205 210 1-2.  
FT REPEAT 279 284 1-3.  
FT REPEAT 410 415 1-4.  
FT REPEAT 635 640 1-5.  
FT REPEAT 674 679 1-6.  
FT DOMAIN 149 172 4 X 6 AA APPROXIMATE TANDEM REPEATS.  
FT REPEAT 149 154 2-1.  
FT REPEAT 155 160 2-2.  
FT REPEAT 161 166 2-3.  
FT REPEAT 167 172 2-4.  
SQ SEQUENCE 928 AA; 101228 MW; 67D45466A4B92390 CRC64;

Query Match 6.0%; Score 180.5; DB 1; Length 928;  
Best Local Similarity 20.6%; Pred. No. 0.058;  
Matches 127; Conservative 92; Mismatches 253; Indels 145; Gaps 22;  
  
QY 35 KTAVLATLLFATVQASANNEEQEEDLYDPVQRTVAVLVIVNSD-----KEGT----- 81  
DB 3 KLVNLSLIILFTCSGAAYASTPDPFHHTVFGTVTIEKTTADKMTIKGSDKAQIDWKS 62  
  
QY 82 ---GEKEKV--BENSQWAVYFNEKGVLTAREITLKAGDNLKI---KQNGTNFTYSLKKDL 133  
DB 63 PDIGQKKEVKFQPNHAYVNRVIGGNASQIQGLTANGKVLNPNPNCVITQGAENY 122  
  
QY 134 TDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTVH-----LNGIGSTLTD- 188  
DB 123 AGLLATTCKDLERISENSNSYQFTRRTKQVLEKGLVLDKGQVKEGVINEGNITAQDF 182  
  
QY 189 TLLNTGATNTVNDVDEKKAASVKDVLNAGNKGKPGCTTASDNVDVFRYTDVE 248  
DB 183 VVLNGDEVINKGNINV---EKNSTINGKVLSSGYNFTFLPDSGIS----- 226  
  
QY 249 FLSADTKTTTVNVEKDKNGKTEVKIGAK-----TSVIKEDGKLVGTG 291  
DB 227 -VALEDNTVQGIKNEGSIKAGEITLSAKGRKQALDSLVMNNGVLEATKVSNNKNGKVLVS 285  
  
QY 292 KDKGE-NGSSTDEGGLVTAKEVIDAVNKAQWRMKTTFANGQTQGAQKPFETVTSNTVF 350  
DB 286 ADNVELNNESTIKGE-IVTFEGADVTSNKLKDNKITSGTSKVTSPKINFTGKSVNING 344  
  
QY 351 ASGKGTATVSKDDOGNTVMTDVNVGDALNVNQL---QNSGNLDSKAVAGSSGKVI 407  
DB 345 NFGREDSTTHYKDFKKLTVENIDVPDNIADIEDNTGTGTG---TGTSSFIQTG 401

QY 408 NYS---PSKGKMD---ETVNI-----NAG-----NNIETIRNGK--- 435  
DB 402 ALSSLLANNGKVNKGNVNNISGRHIDSFRGSDSILLKLTNKGHIDINNADIHSKGRUFF 461  
QY 436 -----NIDIATSMTPQFSSSVSLGAGADAPTLUSDGDAIN-----VSGKKDNKPKVRITN 483  
DB 462 ITSLONEEDFKSNITITDSKINLNGAMGLGRSVDEKDYDNRWQKTEGSRKKKFDVKMSN 521  
QY 484 VAPGVKEGDVTNVAQLKGVAQNLNRRIDNV---DGNARAGIAQAATAGLVQAYLPGKSM 540  
DB 522 VE-----FNQVDDVILAGGFEKVNLDKIVAT-----GQTN 551  
QY 541 MAIGGGTYRGEAGYAIG 557  
DB 552 FYIDGGVSRNGRKYEG 568

Search completed: September 5, 2002, 10:31:09  
Job time: 436 sec

Thu Sep 5 14:36:14 2002

us-09-700-293-4.rsp

Page 14

-----

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:30:29 ; Search time 55.9 Seconds  
(without alignments)  
1828.980 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWNALNAWVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	2999	99.9	591	16	Q9JRL8	Q9JRL8 neisseria m
2	2995	99.7	591	2	Q9JPS7	Q9JPS7 neisseria m
3	2980	99.2	591	2	Q93QX3	Q93QX3 neisseria m
4	2967.5	98.8	592	2	Q9AQF0	Q9AQF0 neisseria m
5	2889.5	96.2	590	2	Q9JPS3	Q9JPS3 neisseria m
6	2762.5	92.0	594	2	Q93QV4	Q93QV4 neisseria m
7	2757.5	91.8	600	2	Q9JPS6	Q9JPS6 neisseria m
8	2751.5	91.6	594	2	Q9JPS3	Q9JPS3 neisseria m
9	2747.5	91.5	594	2	Q9JPS2	Q9JPS2 neisseria m
10	2736.5	91.1	594	2	Q9JPH7	Q9JPH7 neisseria m
11	2734.5	91.1	598	2	Q9JPR9	Q9JPR9 neisseria m
12	2721.5	90.6	598	2	Q9JPT0	Q9JPT0 neisseria m
13	2721.5	90.6	598	2	Q9JPS0	Q9JPS0 neisseria m
14	2712.5	90.3	598	2	Q93QV5	Q93QV5 neisseria m
15	2689	89.5	599	2	Q9JPR8	Q9JPR8 neisseria m
16	2620.5	87.3	592	2	Q9JPS9	Q9JPS9 neisseria m

#### ALIGNMENTS

RESULT 1

ID	Q9JRL8	PRELIMINARY:	PRT:	591 AA.
AC	Q9JRL8;			
DT	01-OCT-2000 (TremBLrel. 15, Created)			
DT	01-OCT-2000 (TremBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TremBLrel. 19, Last annotation update)			
DE	OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).			
GN	GNA992 OR NME0992 OR NHHA.			
OS	Neisseria meningitidis, and			
OS	Neisseria meningitidis (serogroup B).			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487, 491;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;			
RX	MEDLINE=20175756; PubMed=10710308;			
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Huidt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;			
RT	"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";			
RL	Science 287:1816-1820(2000).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / SEROGROUP B;			
RX	MEDLINE=20175755; PubMed=10710307;			
RA	Tettelin H., Saunders N.J., Hood D.W., Peden J.F., Dodson R.J., Eisen J.A., Ketchum K.A., Heide J., Peterson J.D., Hickey E.K., Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Dougherty B.A., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittiore H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,			

Q9JPS8 neisseria m  
Q9JPR7 neisseria m  
Q93QY2 neisseria m  
Q9JPH0 neisseria m  
Q9JPS5 neisseria m  
Q9JPI0 neisseria m  
Q93QY1 neisseria m  
Q9JQW4 neisseria m  
Q9JPS4 neisseria m  
Q9JPS1 neisseria m  
P71401 haemophilus  
Q48152 haemophilus  
Q9F3X6 pasteurella  
Q9PD50 xylella fas  
Q9F2D8 salmonella  
Q9PC04 xylella fas  
Q9F3X5 pasteurella  
Q92KG7 rhizobium m  
Q98HJ2 rhizobium l  
Q9PD63 xylella fas  
Q9F2D8 salmonella  
Q9F2D8 salmonella  
Q916T7 escherichia  
Q9AL50 shigella fl  
Q93TY6 staphylococ  
Q48031 haemophilus  
O54356 moraxella c  
Q98E20 rhizobium l  
Q9RNI2 haemophilus  
Q916T8 escherichia

RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
MC58.";  
RL Science 287:1809-1815(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=N.meningitidis; STRAIN=PMC21;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of *Neisseria meningitidis*";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226375; AAF42524.1;  
DR EMBL: AF202450; AAF41395.1;  
DR EMBL: AF226367; AAF42516.1;  
DR EMBL: AF226370; AAF42519.1;  
DR EMBL: AF226374; AAF42523.1;  
DR EMBL: AF157611; AAF68872.1;  
DR TIGR: NMB0992.  
KW Complete proteome.  
SQ SEQUENCE 591 AA: 62112 MW: 7C22F3CAE7F73EC6 CRC64;

Query Match 99.9%; Score 2999; DB 16; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.9e-118;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60  
DB 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60  
QY 61 YLDPVQRTVAVLIVNSDKGTEGKEKVENSDWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
DB 61 YLDPVQRTVAVLIVNSDKGTEGKEKVENSDWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
QY 121 NGTFYTSLLKDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
DB 121 NGTFYTSLLKDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDLTLLTGATNTVNDVTDDEKRAASVKDVLNAGNWKGVKPGTTASDNVDF 240  
DB 181 GIGSTLTDLTLLTGATNTVNDVTDDEKRAASVKDVLNAGNWKGVKPGTTASDNVDF 240  
QY 241 VRTYDTVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKGLVTGDKGNGSS 300  
DB 241 VRTYDTVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKGLVTGDKGNGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEVTSVGTNVTFAKGGTTATV 360  
DB 301 TDEGGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEVTSVGTNVTFAKGGTTATV 360  
QY 361 SKDDQGNITVMYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGRMDEV 420  
DB 361 SKDDQGNITVMYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGRMDEV 420  
QY 421 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKNPKVR 480  
DB 421 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKNPKVR 480  
QY 481 ITNVPAGVKEGDTNVNQLKGVQVNLNNDVNDGNARAGTAQAIATAGLVQAYLPKSKM 540  
DB 481 ITNVPAGVKEGDTNVNQLKGVQVNLNNDVNDGNARAGTAQAIATAGLVQAYLPKSKM 540  
QY 541 MAIGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRHFHGASVGYQW 591  
DB 541 MAIGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRHFHGASVGYQW 591

RESULT 2  
Q9JFS7 PRELIMINARY; PRT; 591 AA.  
ID Q9JFS7  
AC Q9JFS7  
DT 01-Oct-2000 (TrEMBLrel. 15, Created)  
DT 01-Oct-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarfelli M., Storni E., Zuo P.,  
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1;  
SQ SEQUENCE 591 AA: 62113 MW: 533453CAE5A91E1F CRC64;

Query Match 99.7%; Score 2995; DB 2; Length 591;  
Best Local Similarity 99.7%; Pred. No. 2.8e-118;  
Matches 589; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60  
DB 1 MNKIYRIWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60  
QY 61 YLDPVQRTVAVLIVNSDKGTEGKEKVENSDWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
DB 61 YLDPVQRTVAVLIVNSDKGTEGKEKVENSDWAVYFNEKGVLTAREITLKAGDNLIKQ 120  
QY 121 NGTFYTSLLKDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
DB 121 NGTFYTSLLKDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDLTLLTGATNTVNDVTDDEKRAASVKDVLNAGNWKGVKPGTTASDNVDF 240  
DB 181 GIGSTLTDLTLLTGATNTVNDVTDDEKRAASVKDVLNAGNWKGVKPGTTASDNVDF 240  
QY 241 VRTYDTVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKGLVTGDKGNGSS 300  
DB 241 VRTYDTVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKGLVTGDKGNGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEVTSVGTNVTFAKGGTTATV 360  
DB 301 TDEGGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEVTSVGTNVTFAKGGTTATV 360  
QY 361 SKDDQGNITVMYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGRMDEV 420  
DB 361 SKDDQGNITVMYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGRMDEV 420  
QY 421 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKNPKVR 480  
DB 421 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDKNPKVR 480  
QY 481 ITNVPAGVKEGDTNVNQLKGVQVNLNNDVNDGNARAGTAQAIATAGLVQAYLPKSKM 540  
DB 481 ITNVPAGVKEGDTNVNQLKGVQVNLNNDVNDGNARAGTAQAIATAGLVQAYLPKSKM 540  
QY 541 MAIGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRHFHGASVGYQW 591  
DB 541 MAIGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRHFHGASVGYQW 591

RESULT 3  
Q93QY3 PRELIMINARY; PRT; 591 AA.  
ID Q93QY3  
AC Q93QY3;

DT 01-DEC-2001 (TrEMBLrel. 19; Created)  
DT 01-DEC-2001 (TrEMBLrel. 19; Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19; Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-EG329;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157606; AAK68867.1; --  
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;

Query Match 99.2%; Score 2980; DB 2; Length 591;  
Best Local Similarity 99.3%; Pred. No. 1.2e-117;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATKTAVALTLFLFATVQASANNBQEBDL 60  
Db 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATKTAVALTLFLFATVQASANNBQEBDL 60  
Qy 61 YLDPVQRTAVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLAKGDLNLIK 120  
Db 61 YLDPVLRVAVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLAKGDLNLIK 120  
Qy 121 NGTFTYSLKDLTDLTSVGTGKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGTFTYSLKDLTDLTSVGTGKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
Qy 181 GIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNVDF 240  
Db 181 GIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNVDF 240  
Qy 241 VRTYDTVEFLSADTKTTTVNVESKDKGKTEVIGAKTSVKEKDKGLVTGKDKGENSS 300  
Db 241 VRTYDTVEFLSADTKTTTVNVESKDKGKTEVIGAKTSVKEKDKGLVTGKDKGENSS 300  
Qy 301 TDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTQADKFEFTVSGTNTVFASGKGTATV 360  
Db 301 TDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTQADKFEFTVSGTNTVFASGKGTATV 360  
Qy 361 SKDDGNTVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVTISGNVSPSKGKMDTV 420  
Db 361 SKDDGNTVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVTISGNVSPSKGKMDTV 420  
Qy 421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKDKNPVR 480  
Db 421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKDKNPVR 480  
Qy 481 ITNVAPGVKEGDTVNVQALKGVAQNLRIDNVNDRAGIAQAATATAGLVQAYLPKGS 540  
Db 481 ITNVAPGVKEGDTVNVQALKGVAQNLRIDNVNDRAGIAQAATATAGLVQAYLPKGS 540  
Qy 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591

RESULT 4  
Q9AQF0 PRELIMINARY; PRT; 592 AA.  
AC Q9AQF0;  
DT 01-JUN-2001 (TrEMBLrel. 17; Created)  
DT 01-JUN-2001 (TrEMBLrel. 17; Last sequence update)  
DE OUTER MEMBRANE PROTEIN.  
GN NHHA.

OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MC58;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF125375; AAK09243.1; --  
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 98.8%; Score 2967.5; DB 2; Length 592;  
Best Local Similarity 98.8%; Pred. No. 4e-117;  
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATKTAVALTLFLFATVQASANNBQEBDL 59  
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATKTAVALTLFLFATVQASANNBPRKDD 60  
Qy 60 YLDPVQRTAVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLAKGDLNLIK 119  
Db 61 YLDPVQRTAVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLAKGDLNLIK 120  
Qy 120 QNGTFTYSLKDLTDLTSVGTGKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHL 179  
Db 121 QNGTFTYSLKDLTDLTSVGTGKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHL 180  
Qy 180 NGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNVD 239  
Db 181 NGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTASDNVD 240  
Qy 240 FVRTYDTVEFLSADTKTTTVNVESKDKGKTEVIGAKTSVKEKDKGLVTGKDKGENS 299  
Db 241 FVRTYDTVEFLSADTKTTTVNVESKDKGKTEVIGAKTSVKEKDKGLVTGKDKGENS 300  
Qy 300 STDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTQADKFEFTVSGTNTVFASGKGTAT 359  
Db 301 STDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTQADKFEFTVSGTNTVFASGKGTAT 360  
Qy 360 VSKDDGNTVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVTISGNVSPSKGKMDTV 419  
Db 361 VSKDDGNTVMYDVNVGDALNVNQLNSGWNLDKAVAGSGKVTISGNVSPSKGKMDTV 420  
Qy 420 VNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKDKNPV 479  
Db 421 VNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGALNVGSKDKNPV 480  
Qy 480 RITNVAPGVKEGDTVNVQALKGVAQNLRIDNVNDRAGIAQAATATAGLVQAYLPKGS 539  
Db 481 RITNVAPGVKEGDTVNVQALKGVAQNLRIDNVNDRAGIAQAATATAGLVQAYLPKGS 540  
Qy 540 MMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591  
Db 541 MMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 592

RESULT 5  
Q9JPS3 PRELIMINARY; PRT; 590 AA.  
AC Q9JPS3;  
DT 01-OCT-2000 (TrEMBLrel. 15; Created)  
DT 01-OCT-2000 (TrEMBLrel. 15; Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16; Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.

OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RC STRAIN=NGR28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capecci B.,
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Scorni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT *Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.*;
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match          96.2%; Score 2889.5; DB 2; Length 590;
Best Local Similarity 97.1%; Pred. No. 7.3e-114;
Matches 575; Conservative 4; Mismatches 10; Indels 3; Gaps 2;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLPATVQASANNHEDEDL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLPATVQASANNHEDEED- 59
QY 61 YLDPVORTAVLVNSDKETGCKEKEVENSQWYFNEKGLVLTAREITLKAGDNLKIKQ 120
Db 60 -LDPVORTAVLVNSDKETGCKEKEVENSQWYFNEKGLVLTAREITLKAGDNLKIKQ 118
QY 121 NGTNTFYSLLKDLDTLSVGTETKLSFANGKVNITSDTKGLNFAKETAGTGTTHLN 180
Db 119 NGTNTFYSLLKDLDTLSVGTETKLSFANGKVNITSDTKGLNFAKETAGTGTTHLN 178
QY 181 GIGSTPLDTLTNGTATNTVNDVDEKKRAASVKDVLNAGWNIRKVGKPGTTASDNVDF 240
Db 179 GIGSTPLDTLTNGTATNTVNDVDEKKRAASVKDVLNAGWNIRKVGKPGTTASDNVDF 238
QY 241 VRTYDTEVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVKEKDKGLVTKGKNGSS 300
Db 239 VRTYDTEVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVKEKDKGLVTKGKNGSS 298
QY 301 TDEGEGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGKGTATV 360
Db 299 TDEGEGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGKGTATV 358
QY 361 SKDDGNTVYDNYVDGALNVLQNSGWNLDKAVAGSGKVISGNYSPSKGMDETV 420
Db 359 SKDDGNTVYDNYVDGALNVLQNSGWNLDKAVAGSGKVISGNYSPSKGMDETV 418
QY 421 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSKDKRPV 479
Db 419 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSKDKRPV 478
QY 480 RITNVPQVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQAIATAGLVQAYLPKGS 539
Db 479 RITNVPQVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQAIATAGLVQAYLPKGS 538
QY 540 MMAIGGGTYRGEAGYAGYSSISDGGNWIIRKTASGNSRGRHFGFASASVGYQW 591
Db 539 MMAIGGGTYRGEAGYAGYSSISDGGNWIIRKTASGNSRGRHFGFASASVGYQW 590

RESULT 6
ID Q93QY4 PRELIMINARY; PRT: 594 AA.
AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;

```

```

RN SEQUENCE FROM N.A.
RP STRAIN=EG32;
RC Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RA "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -.
SQ SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;

Query Match          92.0%; Score 2762.5; DB 2; Length 594;
Best Local Similarity 92.5%; Pred. No. 1.5e-108;
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLPATVQASANNHEDEDL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLPATVQASANNHEDEED- 57
QY 61 YLDPVORTAVLVNSDKETGCKEKEVENSQWYFNEKGLVLTAREITLKAGDNLKIKQ 120
Db 58 YLDPVORTAVLVNSDKETGCKEKEVENSQWYFNEKGLVLTAREITLKAGDNLKIKQ 116
QY 121 -----NGTNTFYSLLKDLDTLSVGTETKLSFANGKVNITSDTKGLNFAKETAGTNGD 174
Db 117 NTNENTNASSFTYSLKDLDTLSVGTETKLSFANGKVNITSDTKGLNFAKETAGTNGD 176
QY 175 TTVHLNGIGSTPLDTLTNGTATNTVNDVDEKKRAASVKDVLNAGWNIRKVGKPGTTA 234
Db 177 TTVHLNGIGSTPLDTLTNGTATNTVNDVDEKKRAASVKDVLNAGWNIRKVGKPGTTA 236
QY 235 SDNVDFVTRTYDTEVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVKEKDKGLVTKGDK 294
Db 237 SDNVDFVTRTYDTEVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVKEKDKGLVTKGDK 296
QY 295 GENSSTDEGEGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGK 354
Db 297 GENSSTDEGEGLVTAKEVIDAVNAGWRMKTITANGOTQADKFEFVTSVGTNTVTFASGK 356
QY 355 GTTATVSKDDGNTVYDNYVDGALNVLQNSGWNLDKAVAGSGKVISGNYSPSKG 414
Db 357 GTTATVSKDDGNTVYDNYVDGALNVLQNSGWNLDKAVAGSGKVISGNYSPSKG 416
QY 415 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
Db 417 KMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK 476
QY 474 KDKPVRITVAVPCVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQAIATAGLVQ 533
Db 477 DANKPVRITVAVPCVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQAIATAGLVQ 536
QY 534 YLPKGSMAIGGGTYRGEAGYAGYSSISDGGNWIIRKTASGNSRGRHFGFASASVGYQW 591
Db 537 YLPKGSMAIGGGTYRGEAGYAGYSSISDGGNWIIRKTASGNSRGRHFGFASASVGYQW 594

RESULT 7
ID Q9JPS6 PRELIMINARY; PRT: 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN SEQUENCE FROM N.A.
RP STRAIN=E26;
RC MEDLINE=20175756; PubMed=10710308;
RX Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA

```



RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood E.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RL Meningococcus by Whole-Genome Sequencing.";  
DR EMBL: AF226371; AAF42520.1; -;  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.8%; Score 2757.5; DB 2; Length 600;  
Best Local Similarity 91.5%; Pred. No. 2.5e-108;  
Matches 550; Conservative 14; Mismatches 26; Indels 11; Gaps 3;

Qy 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVAVLATLLFATVQASANN----EEQ 56  
Db 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVAVLATLLFATVQASADN 60  
Qy 57 EEDLYLDPVORTVAVLIVNSDKGEGEKEKEVEENSDWAVYFNEKGVLTAREITLTKAGDNL 116  
Db 61 EEEETLEPVVPTAPVLSYSAEDTGEKE-VTENTNNGIYFDKNGVIKAGTITLTKAGDNL 119  
Qy 117 KIKQ-----NCTNFTYSLKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAG 170  
Db 120 KIKQNTDENTNASFTYSLKELDTLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAG 179  
Qy 171 TNGDTHVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNIKGVKP 230  
Db 180 TNGDTHVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNIKGVKP 239  
Qy 231 GTTASDNVDVFTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 290  
Db 240 GTTASDNVDVFTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 299  
Qy 291 GKDKGENSSYDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGAQDFEIVTSGTNVTF 350  
Db 300 GKDKGENSSYDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGAQDFEIVTSGTNVTF 359  
Qy 351 ASGKGTATVSKDDOGNTVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVS 410  
Db 360 ASGKGTATVSKDDOGNTVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVS 419  
Qy 411 PSKGMDETVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNV 470  
Db 420 PSKGMDETVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNV 479  
Qy 471 GSKDKNKPVRITNVAPVKEGDVTNVAOLKGAQNLLNRRIDNVGNARAGIAQAATAGL 530  
Db 480 GSKDKNKPVRITNVAPVKEGDVTNVAOLKGAQNLLNRRIDNVGNARAGIAQAATAGL 539  
Qy 531 VQAYLPKGSMAIGGGTYRGAGYAGYSSISDGGNWIKTGASGNSRGHGFCASASVGYQ 590  
Db 540 VQAYLPKGSMAIGGGTYRGAGYAGYSSISDGGNWIKTGASGNSRGHGFCASASVGYQ 599  
Qy 591 W 591  
Db 600 W 600

RESULT 8  
Q9JPI3 PRELIMINARY; PRT; 594 AA.  
AC Q9JPI3  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND BZ232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood E.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RL Meningococcus by Whole-Genome Sequencing.";  
DR EMBL: AF226376; AAF42525.1; -;  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 91.6%; Score 2751.5; DB 2; Length 594;  
Best Local Similarity 92.1%; Pred. No. 4.4e-108;  
Matches 551; Conservative 13; Mismatches 23; Indels 11; Gaps 4;

Qy 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVAVLATLLFATVQASANNEEEDL 60  
Db 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVAVLATLLFATVQASTD---DDL 57  
Qy 61 YLDPVORTVAVLIVNSDKGEGEKEKEVEENSDWAVYFNEKGVLTAREITLTKAGDNLKIQ 120  
Db 58 YLDPVORTVAVLIVNSDKGEGEKEKEVEENSDWAVYFNEKGVLTAREITLTKAGDNLKIQ 116  
Qy 121 -----NCTNFTYSLKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGD 174  
Db 117 NTDETNNTSFTYSLKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGD 176  
Qy 175 TTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNIKGVKPGTTA 234  
Db 177 TTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNIKGVKPGTTA 236  
Qy 235 SDNVDFVFTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLVTKDK 294  
Db 237 SDNVDFVFTYDVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLVTKDK 296  
Qy 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGAQDFEIVTSGTNVTFASG 354  
Db 297 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGAQDFEIVTSGTNVTFASG 356  
Qy 355 GTTATVSKDDOGNTVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414  
Db 357 GTTATVSKDDOGNTVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
Qy 415 KMDETVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473  
Db 417 KMDETVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSK 476  
Qy 474 KDKPKVRITNVAPVKEGDVTNVAOLKGAQNLLNRRIDNVGNARAGIAQAATAGLVOA 533  
Db 477 DANKPVRITNVAPVKEGDVTNVAOLKGAQNLLNRRIDNVGNARAGIAQAATAGLVOA 536  
Qy 534 YLPKGSMAIGGGTYRGAGYAGYSSISDGGNWIKTGASGNSRGHGFCASASVGYQW 591  
Db 537 YLPKGSMAIGGGTYRGAGYAGYSSISDGGNWIKTGASGNSRGHGFCASASVGYQW 594  
RESULT 9  
Q9JPS2 PRELIMINARY; PRT; 594 AA.  
AC Q9JPS2  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.

```
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RA PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeanducci C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match          91.5%; Score 2747.5; DB 2; Length 594;
Best Local Similarity 92.0%; Pred. No. 6.5e-108;
Matches 550; Conservative 13; Mismatches 24; Indels 11; Gaps 4;

QY 1 MNKYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60
DB 1 MNKYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 57
QY 61 YLDPVQRTAVVLVNSDKGEGTGEKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIQ 120
DB 58 YLEPVQRTAVVLVNSDKGEGTGEKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIQ 116
QY 121 -----NGTFTYSLAKDLTDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGD 174
DB 117 NTDENTWASSFTYSLAKDLTDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGD 176
QY 175 TTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGNIIKGVKPGTTA 234
DB 177 TTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGNIIKGVKPGTTA 236
QY 235 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDK 294
DB 237 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDK 296
QY 295 GENGSSDTEGEGLVTAKEVIDAVNKAGWRMKTITTTANGOTQADKFFETVSGTNVTFASGK 354
DB 297 GENGSSDTEGEGLVTAKEVIDAVNKAGWRMKTITTTANGOTQADKFFETVSGTNVTFASGK 356
QY 355 GTTATVSKDDQGNITVMDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 414
DB 357 GTTATVSKDDQGNITVMDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 416
QY 415 KMDETVINAGNIIETRNKKNIDTSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 473
DB 417 KMDETVINAGNIIETRNKKNIDTSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 476
QY 474 KDKPVRITINAPGVKEGDVTNVAQLKGVAQNLNRIIDNVDGNARAGIAQAATATAGLVQA 533
DB 477 DANKPVRITINAPGVKEGDVTNVAQLKGVAQNLNRIIDNVDGNARAGIAQAATATAGLVQA 536
QY 534 YLPCKSMATGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGYQW 591
DB 537 YLPCKSMATGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRHFAGASVGYQW 594

RESULT 10
Q9JPH7
ID Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
```

```
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198, AND 297-0;
RA PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeanducci C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match          91.1%; Score 2736.5; DB 2; Length 594;
Best Local Similarity 92.0%; Pred. No. 1.9e-107;
Matches 550; Conservative 11; Mismatches 26; Indels 11; Gaps 4;

QY 1 MNKYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60
DB 1 MNKYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD---DDDL 57
QY 61 YLDPVQRTAVVLVNSDKGEGTGEKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIQ 120
DB 58 YLEPVQRTAVVLVNSDKGEGTGEKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIQ 116
QY 121 -----NGTFTYSLAKDLTDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGD 174
DB 117 NTDENTWASSFTYSLAKDLTDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGD 176
QY 175 TTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGNIIKGVKPGTTA 234
DB 177 TTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGNIIKGVKPGTTA 236
QY 235 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDK 294
DB 237 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDK 296
QY 295 GENGSSDTEGEGLVTAKEVIDAVNKAGWRMKTITTTANGOTQADKFFETVSGTNVTFASGK 354
DB 297 GENGSSDTEGEGLVTAKEVIDAVNKAGWRMKTITTTANGOTQADKFFETVSGTNVTFASGK 356
QY 355 GTTATVSKDDQGNITVMDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 414
DB 357 GTTATVSKDDQGNITVMDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 416
QY 415 KMDETVINAGNIIETRNKKNIDTSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 473
DB 417 KMDETVINAGNIIETRNKKNIDTSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 476
QY 474 KDKPVRITINAPGVKEGDVTNVAQLKGVAQNLNRIIDNVDGNARAGIAQAATATAGLVQA 533
DB 477 DANKPVRITINAPGVKEGDVTNVAQLKGVAQNLNRIIDNVDGNARAGIAQAATATAGLVQA 536
```

```
Qy 534 YLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGRHGFGASASVGYQW 591
|||||
Db 537 YLPKSMMAIGDTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGRHGFGASASVGYQW 594
|||||

RESULT 11
QJUPR9
ID QJUPR9 PRELIMINARY; PRT; 598 AA.
AC QJUPR9;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 91.1%; Score 2734.5; DB 2; Length 598;
Best Local Similarity 91.4%; Pred. No. 2.3e-107;
Matches 550; Conservative 11; Mismatches 26; Indels 15; Gaps 4;

Qy 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVOASANNEQEDL 60
|||||
Db 1 MNKIYRIIWNLSALNAWVVSELTRNHTKRASATVATVATLTLFATVOANATD---DDDL 57
|||||

Qy 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
|||||
Db 58 YLEPQRTAVLVLSFRSDKEGTGEKTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIQ 116
|||||

Qy 121 -----NCTNTYSLLKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAG 170
|:|||||
Db 117 NTNENTNENTDSSFTYSLKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAG 176
|:|||||

Qy 171 TNGDPTVHLNGTSLTDTLLNTGATVNTNDVDDDEKRAASVKDVLNAGNIIKGVKP 230
|||||
Db 177 TNGDPTVHLNGTSLTDTLLNTGATVNTNDVDDDEKRAASVKDVLNAGNIIKGVKP 236
|||||

Qy 231 GTTASDNVDVFRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIEKDGKLV 290
|||||
Db 237 GTTASDNVDVFRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIEKDGKLV 296
|||||

Qy 291 GKDKGENSSDTEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKPEFTVSGTNVTF 350
|||||
Db 297 GKDKGENSSDTEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKPEFTVSGTNVTF 356
|||||

Qy 351 ASGKGTATVSKDDOGNTVYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVS 410
|||||
Db 357 ASGKGTATVSKDDOGNTVYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVS 416
|||||

Qy 411 PSKGMDETVINAGNIIETRNKNIDTATSMTPQFSSVSLGAGADAPTLSVDGD-ALN 469
|||||
Db 417 PSKGMDETVINAGNIIETRNKNIDTATSMTPQFSSVSLGAGADAPTLSVDDEGALN 476
|||||

Qy 470 VGSKKDNKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDNVQNALAGTAIAATAG 529
|||||
```

```
Db 477 VGSKDNKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDNVQNALAGTAIAATAG 536
|||||
Qy 530 LVOAYLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGRHGFGASASVGY 589
|||||
Db 537 LVOAYLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGRHGFGASASVGY 596
|||||

Qy 590 QW 591
|||
Db 597 QW 598
|||

RESULT 12
QJUPR9
ID QJUPR9 PRELIMINARY; PRT; 598 AA.
AC QJUPR9;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;
```

```
Query Match 90.6%; Score 2721.5; DB 2; Length 598;
Best Local Similarity 90.7%; Pred. No. 8e-107;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

Qy 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVATVATLTLFATVOASANNEQEDL 60
|||||
Db 1 MNKIYRIIWNLSALNAWVVSELTRNHTKRASATVATVATLTLFATVOANATD---DDDL 57
|||||

Qy 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
|||||
Db 58 YLEPQRTAVLVLSFRSDKEGTGEKTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIQ 116
|||||

Qy 121 -----NCTNTYSLLKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAG 170
|:|||||
Db 117 NTNENTNENTDSSFTYSLKDLTDLTSVTEKLSFGANGKVNITSDTKGLNFAKETAG 176
|:|||||

Qy 171 TNGDPTVHLNGTSLTDTLLNTGATVNTNDVDDDEKRAASVKDVLNAGNIIKGVKP 230
|||||
Db 177 TNGDPTVHLNGTSLTDTLLNTGATVNTNDVDDDEKRAASVKDVLNAGNIIKGVKP 236
|||||

Qy 231 GTTASDNVDVFRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIEKDGKLV 290
|||||
Db 237 GTTASDNVDVFRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIEKDGKLV 296
|||||

Qy 291 GKDKGENSSDTEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKPEFTVSGTNVTF 350
|||||
Db 297 GKDKGENSSDTEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKPEFTVSGTNVTF 356
|||||

Qy 351 ASGKGTATVSKDDOGNTVYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVS 410
|||||
Db 357 ASGKGTATVSKDDOGNTVYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVS 416
|||||
```

```

QY 411 PSKGMDETNNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVGDG-ALN 469
DB 417 PSKGMDETNNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALN 476
QY 470 VGSKKDNKPVRIITNVAPGVEGDTNVNLAQLGVAQNINNRIDNVGNARAGIAQAIAATAG 529
DB 477 VGSKKDNKPVRIITNVAPGVEGDTNVNLAQLGVAQNINNRIDNVGNARAGIAQAIAATAG 536
QY 530 LVQAYLPCKSMAIIGGTYRGEAGYAIGYSSISDGGNWIIGKTASNSRGHFGCASVGY 589
DB 537 LAQAYLPCKSMAIIGGTYRGEAGYAIGYSSISDTGNWVIGKTASNSRGHFGTASVGY 596
QY 590 QW 591
DB 597 QW 598

RESULT 13
QJPSO
ID QJPSO PRELIMINARY; PRT; 598 AA.
AC QJPSO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HL5;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226381; AAF42530.1; -.
DR EMBL; AF157607; AAK68868.1; -.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;

Query Match 90.6%; Score 2721.5; DB 2; Length 598;
Best Local Similarity 90.9%; Pred. No. 8e-107;
Matches 547; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKIYRIWNSALNNAVVSSELTRNHTKRASATVKTAVLATLFAVQASANNNEQEDL 60
DB 1 MNKIYRIWNSALNNAVVSSELTRNHTKRASATVATATLFAVQANATD---DDDL 57
QY 61 YLDPVQRTAVLVNSDKEGTGEKEKVEENSDWAVYENKGVLTAREITLKAGDNLIKQ 120
DB 58 YLEVPQRTAVLVNSDKEGTGEKEGTD-SNWAVYFDEKRVLKAGITLKAGDNLIKQ 116
QY 121 -----NGNTFTYSLKDLTDLTSVGTKEKLSFSAANGKNVITSDDTKGLNFAKETAG 170
DB 117 NTNENTNENTNDSSTFTYSLKDLTDLTSVETKEKLSFGANGKNVITSDDTKGLNFAKETAG 176
QY 171 TNGDTTVHLNGIGSTLTDPLLTGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVP 230
DB 177 TNGDPTVHLNGIGSTLTDPLLTGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVP 236

```

```

DB 177 TNGDPTVHLNGIGSTLTDPLLTGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVP 236
QY 231 GTTASDNVDFVRYDIVEFLSADTKTTTVNVESKDNKGKTEVKIGARTSVIKEKGKLVY 290
DB 237 GTTASDNVDFVRYDIVEFLSADTKTTTVNVESKDNKGKTEVKIGARTSVIKEKGKLVY 296
QY 291 GKDKGENSGSTDEGEGLVTAKEVIDAVNKGAGRMKTTTANGOTQOAKFETVTSSTNTVF 350
DB 297 GKDKGENSGSTDEGEGLVTAKEVIDAVNKGAGRMKTTTANGOTQOAKFETVTSSTNTVF 356
QY 351 ASGKGTATATVSKDDOQNIITVMYDMVNGDALNVNOLNSGNWLDKSAVASSGKVTSGNVS 410
DB 357 ASGKGTATATVSKDDOQNIITVMYDMVNGDALNVNOLNSGNWLDKSAVASSGKVTSGNVS 416
QY 411 PSKGMDETNNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVGDG-ALN 469
DB 417 PSKGMDETNNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALN 476
QY 470 VGSKKDNKPVRIITNVAPGVEGDTNVNLAQLGVAQNINNRIDNVGNARAGIAQAIAATAG 529
DB 477 VGSKKDNKPVRIITNVAPGVEGDTNVNLAQLGVAQNINNRIDNVGNARAGIAQAIAATAG 536
QY 530 LVQAYLPCKSMAIIGGTYRGEAGYAIGYSSISDGGNWIIGKTASNSRGHFGCASVGY 589
DB 537 LAQAYLPCKSMAIIGGTYRGEAGYAIGYSSISDTGNWVIGKTASNSRGHFGCASVGY 596
QY 590 QW 591
DB 597 QW 598

RESULT 14
QJPSO
ID QJPSO PRELIMINARY; PRT; 598 AA.
AC QJPSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BL210;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157603; AAK68864.1; -.
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 90.3%; Score 2712.5; DB 2; Length 598;
Best Local Similarity 90.5%; Pred. No. 1.9e-106;
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNKIYRIWNSALNNAVVSSELTRNHTKRASATVKTAVLATLFAVQASANNNEQEDL 60
DB 1 MNKIYRIWNSALNNAVVSSELTRNHTKRASATVATATLFAVQANATD---DDDL 57
QY 61 YLDPVQRTAVLVNSDKEGTGEKEKVEENSDWAVYENKGVLTAREITLKAGDNLIKQ 120
DB 58 YLEVPQRTAVLVNSDKEGTGEKEGTD-SNWAVYFDEKRVLKAGITLKAGDNLIKQ 116
QY 121 -----NGNTFTYSLKDLTDLTSVGTKEKLSFSAANGKNVITSDDTKGLNFAKETAG 170
DB 117 NTNENTNENTNDSSTFTYSLKDLTDLTSVETKEKLSFGANGKNVITSDDTKGLNFAKETAG 176
QY 171 TNGDTTVHLNGIGSTLTDPLLTGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVP 230
DB 177 TNGDPTVHLNGIGSTLTDPLLTGATNTVNDVTDDEKKRAASVKDVLNAGWNITKGVP 236

```

[illegible]

Search completed: September 5, 2002, 10:30:31  
Job time: 433 sec

Query Match 89.5%; Score 2689; DB 2; Length 599;  
Best Local Similarity 89.5%; Pred. No. 1.8e-105;  
Matches 539; Conservative 16; Mismatches 33; Indels 1

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:46 ; Search time 25.63 Seconds  
(without alignments)  
563.228 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKYRIIWSALNANWAVS.....TASGNSRGHFCASVGVQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2999	99.9	591	US-09-377-155-21	Sequence 21, Appl
2	2999	99.9	591	US-09-377-155-21	Sequence 11, Appl
3	2980	99.2	591	US-09-377-155-11	Sequence 11, Appl
4	2980	99.2	591	US-09-669-974-11	Sequence 11, Appl
5	2967.5	98.8	592	US-09-377-155-2	Sequence 2, Appl
6	2967.5	98.8	592	US-09-669-974-2	Sequence 2, Appl
7	2762.5	92.0	594	US-09-377-155-9	Sequence 9, Appl
8	2762.5	92.0	594	US-09-669-974-9	Sequence 9, Appl
9	2736.5	91.1	594	US-09-377-155-7	Sequence 7, Appl
10	2736.5	91.1	594	US-09-669-974-7	Sequence 7, Appl
11	2721.5	90.6	598	US-09-377-155-13	Sequence 13, Appl
12	2721.5	90.6	598	US-09-669-974-13	Sequence 13, Appl
13	2712.5	90.3	598	US-09-377-155-5	Sequence 5, Appl
14	2712.5	90.3	598	US-09-669-974-5	Sequence 5, Appl
15	2689	89.5	599	US-09-377-155-15	Sequence 15, Appl
16	2689	89.5	599	US-09-669-974-15	Sequence 15, Appl
17	2577.5	85.8	592	US-09-377-155-17	Sequence 17, Appl
18	2577.5	85.8	592	US-09-669-974-17	Sequence 17, Appl
19	2475	82.4	589	US-09-377-155-19	Sequence 19, Appl
20	2475	82.4	589	US-09-669-974-19	Sequence 19, Appl
21	1245	41.5	2411	US-09-268-347-36	Sequence 36, Appl
22	1243	41.4	2353	US-09-377-155-33	Sequence 33, Appl
23	1243	41.4	2353	US-08-913-942-4	Sequence 4, Appl
24	1243	41.4	2353	US-09-669-974-33	Sequence 33, Appl
25	1242	41.4	2354	US-09-268-347-47	Sequence 47, Appl
26	1180.5	39.3	607	US-08-409-995-6	Sequence 6, Appl
27	1180.5	39.3	607	US-08-685-467-6	Sequence 6, Appl

28	1180.5	39.3	607	4	US-08-913-942-6	Sequence 6, Appl
29	1180.5	39.3	1912	1	US-08-409-995-4	Sequence 4, Appl
30	1180.5	39.3	1912	3	US-08-685-467-4	Sequence 4, Appl
31	1070.5	35.6	1094	4	US-09-268-347-32	Sequence 32, Appl
32	1057.5	35.2	1098	1	US-08-409-995-2	Sequence 2, Appl
33	1057.5	35.2	1098	3	US-08-685-467-2	Sequence 2, Appl
34	1057.5	35.2	1098	4	US-09-377-155-32	Sequence 32, Appl
35	1057.5	35.2	1098	4	US-08-913-942-2	Sequence 2, Appl
36	1057.5	35.2	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1057.5	35.2	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1039.5	34.6	658	1	US-08-409-995-5	Sequence 5, Appl
39	1039.5	34.6	658	3	US-08-685-467-5	Sequence 5, Appl
40	1039.5	34.6	658	4	US-08-913-942-5	Sequence 15, Appl
41	995	33.1	679	4	US-08-913-942-15	Sequence 15, Appl
42	995	33.1	679	4	US-09-268-347-26	Sequence 26, Appl
43	752.5	25.1	1004	4	US-09-268-347-30	Sequence 30, Appl
44	741.5	24.7	1002	4	US-09-268-347-24	Sequence 24, Appl
45	696.5	23.2	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-21  
Sequence 21, Application US/09377155  
Patent No. 6199346  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 21  
LENGTH: 591  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match	99.9%	Score 2999;	DB 4;	Length 591;
Best Local Similarity	99.8%	Pred. No. 6.7e-225;		
Mismatches	590;	Conservative	0;	Mismatches 1; Indels 0; Gaps
Qy	1	MNKYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLTFATVQASANNEQEDL	60	
Db	1	MNKYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLTFATVQASANNEQEDL	60	
Qy	61	YLDPVQRTAVLIIVNSDKEGTEKEVEENSDMAVYNEKGVLTAREITLKAGNLKIQ	120	
Db	61	YLDPVQRTAVLIIVNSDKEGTEKEVEENSDMAVYNEKGVLTAREITLKAGNLKIQ	120	
Qy	121	NGTFTYSLKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN	180	
Db	121	NGTFTYSLKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN	180	
Qy	181	GIGSTLDTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNWKIKVPGTTASDNVDF	240	
Db	181	GIGSTLDTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNWKIKVPGTTASDNVDF	240	
Qy	241	VRTYDTVEFLSADTKTTIVNVESKDKGKTEVKIGAKTSVKEKDKGLVTKDKGNGSS	300	
Db	241	VRTYDTVEFLSADTKTTIVNVESKDKGKTEVKIGAKTSVKEKDKGLVTKDKGNGSS	300	
Qy	301	TDEGGLYTAKEVIDAVNKGAWRMKTTTANTQGTQADKFETVTSCTNVTFASGKGTATV	360	

THIS PAGE BLANK (USPTO)



BEST AVAILABLE COPY

Db 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFAAGKGTATV 360  
QY 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGKMDTV 420  
Db 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
Db 421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
QY 481 ITNVPAGVKEGDVTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIATAGLVOAYLPCKSM 540  
Db 481 ITNVPAGVKEGDVTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIATAGLVOAYLPCKSM 540  
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKTGTASGNSRHFHGASASVGYOW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKTGTASGNSRHFHGASASVGYOW 591

RESULT 2

US-09-669-974-21  
; Sequence 51, Application US/09/669/974  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 99.9%; Score 2999; DB 4; Length 591;  
Best Local Similarity 99.8%; Pred. No. 6.7e-225;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
QY 61 YLDPVQRTVAVLVNSDKETGEGEKEKEEENSDWAVFNEKGVLTAREITLKAGDNLKIQ 120  
Db 61 YLDPVQRTVAVLVNSDKETGEGEKEKEEENSDWAVFNEKGVLTAREITLKAGDNLKIQ 120  
QY 121 NGNTFTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGNTFTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDLLTGATNTVNDNVDDEKKRAASVKDVLNAGNWKGVKPGTTASNDVDF 240  
Db 181 GIGSTLTDLLTGATNTVNDNVDDEKKRAASVKDVLNAGNWKGVKPGTTASNDVDF 240  
QY 241 VRTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGDKGENGSS 300  
Db 241 VRTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGDKGENGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFAAGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFAAGKGTATV 360

Db 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFAAGKGTATV 360  
QY 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGKMDTV 420  
Db 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
Db 421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480  
QY 481 ITNVPAGVKEGDVTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIATAGLVOAYLPCKSM 540  
Db 481 ITNVPAGVKEGDVTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIATAGLVOAYLPCKSM 540  
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKTGTASGNSRHFHGASASVGYOW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKTGTASGNSRHFHGASASVGYOW 591

RESULT 3

US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 99.2%; Score 2980; DB 4; Length 591;  
Best Local Similarity 99.3%; Pred. No. 2e-223;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
Db 1 MNEILRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
QY 61 YLDPVQRTVAVLVNSDKETGEGEKEKEEENSDWAVFNEKGVLTAREITLKAGDNLKIQ 120  
Db 61 YLDPVQRTVAVLVNSDKETGEGEKEKEEENSDWAVFNEKGVLTAREITLKAGDNLKIQ 120  
QY 121 NGNTFTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGNTFTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDLLTGATNTVNDNVDDEKKRAASVKDVLNAGNWKGVKPGTTASNDVDF 240  
Db 181 GIGSTLTDLLTGATNTVNDNVDDEKKRAASVKDVLNAGNWKGVKPGTTASNDVDF 240  
QY 241 VRTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGDKGENGSS 300  
Db 241 VRTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGDKGENGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFAAGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFAAGKGTATV 360  
QY 361 SKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGKMDTV 420

THIS PAGE BLANK (USPTO)